

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 64.2353 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-2

Perfect score: 584

Sequence: 1 DIYVTSPLSLPVTGEPAS.....CMQAQSPITFGGQTRLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	584	100.0	112	7	ADC99773 Anti-huma
2	584	100.0	112	7	ADD05377
3	584	100.0	112	7	ADF09815 Human ant
4	556	95.2	112	8	ADI22130 Anti-plat
5	554	94.9	112	7	ADE28441 Human ant
6	554	94.9	239	7	ADE28465 Human ant
7	553	94.7	112	8	ADI22127 Anti-plat
8	553	94.7	112	8	ADI22112 Anti-plat
9	552	94.5	112	8	ADI22111 Anti-plat
10	552	94.5	112	8	ADI22123 Anti-plat
11	551	94.3	112	8	ADI22124 Anti-plat
12	550	94.2	112	2	AAW53586 Light cha
13	549.5	94.1	113	8	ADI22126 Anti-plat
14	548	93.8	112	7	ADJ76892 Anti-IGF-
15	548	93.8	112	8	ADI22128 Anti-plat
16	548	93.8	112	8	ADO07297 Human pro
17	548	93.8	113	7	ADJ80417 Hybrid hu
18	548	93.8	113	8	ADP47297 Human pho
19	548	93.8	125	5	ABG76926 Humanised
20	548	93.8	125	8	ADR88410 Human pro
21	546	93.5	112	6	ABR55794 Kappa cha
22	546	93.5	112	6	ABR55786 Kappa cha
23	546	93.5	112	7	ADP03893 Murine-ex
24	545.5	93.4	113	8	ADI22125 Anti-plat
25	545	93.3	112	8	ADI22118 Anti-plat

26	545	93.3	112	8	ADI22129
27	545	93.3	112	8	ADI22114
28	545	93.3	112	8	ADL93568 Human CD4
29	545	93.3	238	8	ADL93650 Human CD4
30	544.5	93.2	248	4	AAG65590 Anti-hbDR
31	544	93.2	112	8	ADI22119 Anti-plat
32	543.5	93.1	112	8	ADP47300 Human pho
33	543.5	93.1	113	3	AAV95221 Anti-plat
34	542.5	92.9	111	3	AAV95225 Anti-plat
35	542.5	92.9	112	3	AAV95187 Anti-plat
36	542.5	92.9	113	3	AAV95220 Anti-plat
37	542.5	92.9	114	3	AAV95186 Anti-plat
38	542.5	92.9	131	3	AAV95226 Anti-plat
39	542	92.8	112	7	ADE28487 Human ant
40	542	92.8	112	7	ADE28445 Human ant
41	542	92.8	112	7	ADE28409 Human ant
42	542	92.8	112	7	ADE28425 Human ant
43	542	92.8	112	8	ADI22113 Anti-plat
44	542	92.8	112	8	ADL93580 Human CD4
45	542	92.8	238	8	ADL93654 Human CD4

#### ALIGNMENTS

##### RESULT 1

ADC99773

ID ADC99773 standard; protein; 112 AA.

XX AC ADC99773;

XX AC ADC99773;

DT 01-JAN-2004 (first entry)

XX AC ADC99773;

DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 2.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human.

XX Homo sapiens.

XX Homo sapiens.

PN WO2003057838-A2.

XX 17-JUL-2003.

XX 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

DR N-PSDB; ADC99775.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease

or condition associated with expression of MUC18 in a patient, e.g.

tumors, cancers, and other malignancies.

PT Claim 3; SEQ ID NO 2; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising

a heavy or light chain amino acid or a heavy or light chain variable

domain where the antibody binds to MUC18. The monoclonal antibody of the

invention demonstrates cytostatic activity and may be useful for treating

a disease or condition associated with the expression of MUC18 on the

cell surface such as tumours, specifically melanoma, oesophageal,

pancreatic or colorectal tumours, carcinomas, particularly cervical

carcinomas and cervical intraepithelial neoplasia and cancers including

colorectal, breast or lung cancer, as well as other malignancies. The

current sequence is that of the anti-human MUC18 monoclonal antibody

CC light chain protein of the invention.  
 XX Sequence 112 AA;  
 SQ

Query Match 100.0%; Score 584; DB 7; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 4e-40;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60  
 Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112  
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112

RESULT 2  
 ADD05377  
 ID ADD05377 standard; protein; 112 AA.  
 XX  
 AC ADD05377;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 2.  
 XX  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057006-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041582.  
 XX  
 PR 28-DEC-2001; 2001US-0346460P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J, Bar-Eli M;  
 XX  
 DR WPI; 2003-577496/54.  
 DR N-PSDB; ADD05379.  
 XX

Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumor.

Claim 3; SEQ ID NO 2; 87pp; English.

The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region, protein of the invention.

Sequence 112 AA;  
 Query Match 100.0%; Score 584; DB 7; Length 112;

Best Local Similarity 100.0%; Pred. No. 4e-40;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60  
 Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112  
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112

RESULT 3  
 ADF09815  
 ID ADF09815 standard; protein; 112 AA.  
 XX  
 AC ADF09815;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody light chain #1.  
 XX  
 KW cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; light chain; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057837-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041580.  
 XX  
 PR 28-DEC-2001; 2001US-0346414P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-598367/56.  
 DR N-PSDB; ADF09817.  
 XX

Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.

Claim 3; SEQ ID NO 2; 83pp; English.

The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific monoclonal antibody.

Sequence 112 AA;  
 Query Match 100.0%; Score 584; DB 7; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 4e-40;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60  
 Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112  
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTLEIK 112

RESULT 4  
ADI22130  
ADI22130 standard; protein; 112 AA.  
XX ADI22130;  
AC ADI22130;  
XX  
XX  
XX 22-APR-2004 (first entry)  
DT  
XX  
XX Anti-platelet autoantibody related light chain amino acid L54 SEQ:93.  
DE  
XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;  
XX thrombus; platelet adhesion inhibition;  
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;  
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;  
KW thrombolytic; human.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX WO2004005890-A2.  
XX  
XX 15-JAN-2004.  
XX  
XX 03-JUL-2003; 2003WO-US021304.  
XX  
XX 03-JUL-2002; 2002US-0394352P.  
XX  
XX 18-SEP-2002; 2002US-0411694P.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
XX Siegel DL;  
XX  
XX WPI: 2004-142998/14.  
XX  
XX N-PSDB; ADI22077.  
XX  
XX  
XX Claim 12; SEQ ID NO 93; 232pp; English.  
XX  
XX The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H414 anti-platelet autoantibody; the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic

CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.  
XX  
XX  
XX Sequence 112 AA;  
Query Match 95.2%; Score 556; DB 8; Length 112;  
Best Local Similarity 94.6%; Pred. No. 7.6e-38;  
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DIVVTQSPISLPVTPGEPASISCRSSQSLRSNGYLDWYLOKPGQSPHLLIYLSNRA 60  
DB 1 DIVVTQSPISLPVTPGEPASISCRSSQSLRSNGYLDWYLOKPGQSPHLLIYLSNRA 60  
QY 61 SGVPDRFSGSGGTFTLKISRVEAEDVGYVYCMQAQDSPTFGQGRLLDI 111  
DB 61 SGVPDRFSGSGGTFTLKISRVEAEDVGYVYCMQAQDSPTFGQGRLLDI 111  
RESULT 5  
ADE28441  
ID ADE28441 standard; protein; 112 AA.  
XX  
XX AC ADE28441;  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Human anti-CD40 antibody 21-4-1 full length light chain protein.  
XX  
XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
XX bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
XX human; light chain; 21-4-1.  
XX  
XX Homo sapiens.  
XX  
XX WO2003040170-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 08-NOV-2002; 2002WO-US036107.  
XX  
XX 09-NOV-2001; 2001US-0348980P.  
XX  
XX (PFIZ ) PFIZER PROD INC.  
XX (ABGE-) ABGENIX INC.  
XX  
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
XX  
XX WPI: 2003-441521/41.  
XX N-PSDB; ADE28440.  
XX  
XX New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.  
XX  
XX Claim 7; SEQ ID NO 48; 177pp; English.  
XX  
XX The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length light chain protein of the invention.  
XX  
XX Sequence 112 AA;





CC and an instructions for use. (I) has haemostatic, anticoagulant and  
 CC thrombolytic activities. The autoantibodies (I) are useful for diagnosing  
 CC and for developing therapeutics for diseases mediated by autoantibody  
 CC binding with platelet antigens. (M6) and (M12) are useful for treating  
 CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic  
 CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood  
 CC clotting. The present sequence is used in the exemplification of the  
 CC present invention.

XX Sequence 112 AA;

Query Match 94.7%; Score 553; DB 8; Length 112;  
 Best Local Similarity 94.6%; Pred. No. 1.3e-37;  
 Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

DB 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSHRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQSQSPITFGQTRLEIK 112

DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQSQSPITFGQTRLEIK 112

# RESULT 8

AD122112  
 ID AD122112 standard; protein; 112 AA.

XX AC AD122112;

XX DT 22-APR-2004 (first entry)

XX DE Anti-platelet autoantibody related light chain amino acid L36 SEQ.75.

XX KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;

XX KW thrombus; platelet adhesion inhibition;

XX KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;

XX KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;

XX KW thrombolytic; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX XX WO2004005890-A2.

XX XX 15-JAN-2004.

XX XX 03-JUL-2003; 2003WO-US021304.

XX XX 03-JUL-2002; 2002US-0394352P.

XX XX 18-SEP-2002; 2002US-0411694P.

XX XX (UYPE-) UNIV PENNSYLVANIA.

XX XX Siegel DL;

XX XX WPI; 2004-142998/14.

XX XX N-PSDB; AD122059.

XX XX Claim 12; SEQ ID NO 75; 232pp; English.

XX The present invention describes a method (M1) for identifying an anti-  
 CC platelet autoantibody (I) in a mammal. The autoantibody is detected by  
 CC producing an antibody phage display library from B-lymphocytes obtained  
 CC from the mammal, and screening the library to detect a phage that  
 CC specifically binds with a platelet component, where the screening  
 CC comprises panning the phage on intact platelets using competitive cell-  
 CC surface panning. Also described: (1) an autoantibody identified by (M1);  
 CC (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3)  
 CC inhibiting (M2) blood clotting in a mammal having a thrombus or at risk  
 CC of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a  
 CC mammal having a thrombus or at risk of thrombus formation; (5) inhibiting  
 CC (M4) binding of an anti-platelet autoantibody with a platelet component;

CC (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6)  
 CC thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)  
 CC platelet aggregation; (9) inhibiting (M8) platelet activation; (10)  
 CC inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an  
 CC anti-platelet autoantibody, or its biologically active fragment with a  
 CC platelet; (12) identifying (M11) a peptide that inhibits binding of an  
 CC anti-platelet autoantibody with a platelet; (13) a peptide identified by  
 CC the method of (12); (14) a peptide that specifically binds with an anti-  
 CC platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic  
 CC purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood  
 CC clotting, inhibiting platelet aggregation, inhibiting platelet function  
 CC or inhibiting platelet activation comprising an amount of an anti-  
 CC platelet autoantibody, or its biologically active fragment that  
 CC specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or  
 CC its fragment comprises an antigen binding region derived from an H44L4  
 CC anti-platelet autoantibody, the kit further comprising a peptide  
 CC inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator  
 CC and an instructions for use. (I) has haemostatic, anticoagulant and  
 CC thrombolytic activities. The autoantibodies (I) are useful for diagnosing  
 CC and for developing therapeutics for diseases mediated by autoantibody  
 CC binding with platelet antigens. (M6) and (M12) are useful for treating  
 CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic  
 CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood  
 CC clotting. The present sequence is used in the exemplification of the  
 CC present invention.

XX SQ Sequence 112 AA;

Query Match 94.7%; Score 553; DB 8; Length 112;

Best Local Similarity 94.6%; Pred. No. 1.3e-37;

Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

DB 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQSQSPITFGQTRLEIK 112

DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCMQAQSQSPITFGQTRLEIK 112

# RESULT 9

AD122111  
 ID AD122111 standard; protein; 112 AA.

XX AC AD122111;

XX DT 22-APR-2004 (first entry)

XX DE Anti-platelet autoantibody related light chain amino acid L35 SEQ.74.

XX KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;

XX KW thrombus; platelet adhesion inhibition;

XX KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;

XX KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;

XX KW thrombolytic; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX XX WO2004005890-A2.

XX XX 15-JAN-2004.

XX XX 03-JUL-2003; 2003WO-US021304.

XX XX 03-JUL-2002; 2002US-0394352P.

XX XX 18-SEP-2002; 2002US-0411694P.

XX XX (UYPE-) UNIV PENNSYLVANIA.

XX XX Siegel DL;

XX XX

DR WPI; 2004-142998/14.  
 DR N-PSDB; ADI22058.  
 XX  
 PS Claim 12; SEQ ID NO 74; 232pp; English.  
 XX  
 CC The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H44L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 112 AA;  
 Query Match 94.5%; Score 552; DB 8; Length 112;  
 Best Local Similarity 94.6%; Pred. No. 1.6e-37;  
 Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DIVMTQSPSLPVTGPGEPAISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLGNSRA 60  
 DB 1 DIVMTQSPSLPVTGPGEPAISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLGNSRA 60  
 QY 61 SGVDPFRSGSGGTDTFLKISRVEAEDGVVYCMQAQSPITFGGTRLEIK 112  
 DB 61 SGVDPFRSGSGGTDTFLKISRVEAEDGVVYCMQAQSPITFGGTRLEIK 112

RESULT 10  
 ADI22123  
 ID ADI22123 standard; protein; 112 AA.  
 XX  
 AC ADI22123;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Anti-platelet autoantibody related light chain amino acid L47 SEQ:86.  
 KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;  
 KW thrombus; platelet adhesion inhibition;  
 KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;  
 KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;  
 KW thrombolytic; human.

XX OS Homo sapiens.  
 OS Synthetic.  
 XX WO2004005890-A2.  
 XX 15-JAN-2004.  
 XX 03-JUL-2003; 2003WO-US021304.  
 XX 03-JUL-2002; 2002US-0394352P.  
 XX 18-SEP-2002; 2002US-0411694P.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Siegel Du;  
 XX WPI; 2004-142998/14.  
 DR N-PSDB; ADI22070.  
 DR  
 PS Claim 12; SEQ ID NO 86; 232pp; English.  
 XX  
 CC The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H44L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 112 AA;  
 Query Match 94.5%; Score 552; DB 8; Length 112;  
 Best Local Similarity 95.5%; Pred. No. 1.6e-37;  
 Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DIVMTQSPSLPVTGPGEPAISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLGNSRA 60  
 DB 1 DIVMTQSPSLPVTGPGEPAISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLGNSRA 60  
 QY 61 SGVDPFRSGSGGTDTFLKISRVEAEDGVVYCMQAQSPITFGGTRLEIK 112  
 DB 61 SGVDPFRSGSGGTDTFLKISRVEAEDGVVYCMQAQSPITFGGTRLEIK 112

RESULT 11  
ADI22124  
ID ADI22124 standard; protein; 112 AA.  
XX  
AC ADI22124;  
XX  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Anti-platelet autoantibody related light chain amino acid L48 SEQ:87.  
XX  
XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;  
KW thrombus; platelet adhesion inhibition;  
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;  
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;  
KW thrombolytic; human.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO2004005890-A2.  
XX  
XX 15-JAN-2004.  
XX  
XX 03-JUL-2003; 2003WO-US021304.  
XX  
XX 03-JUL-2002; 2002US-0394352P.  
PR 18-SEP-2002; 2002US-0411694P.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
PA  
XX Siegel DL;  
PI  
XX WPI: 2004-142998/14.  
DR N-PSDB; ADI22071.  
XX  
XX  
PS Claim 12; SEQ ID NO 87; 232pp; English.  
XX  
XX The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H4L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic

CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.  
CC  
XX  
SQ Sequence 112 AA;  
Query Match 94.3%; Score 551; DB 8; Length 112;  
Best Local Similarity 94.8%; Pred. No. 1.9e-37;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DIVMTQSPISLPVTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60  
DB 1 DIVMTQSPISLPVTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60  
QY 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVYCMQAQSPITFGQGRLEIK 112  
DB 61 SGVPDRFSGSGGTFTLKISRVEAEDVGVYCMQAQSPITFGQGRLEIK 112  
RESULT 12  
AAW53586  
ID AAW53586 standard; protein; 112 AA.  
XX  
AC AAW53586;  
XX  
DT 23-JUL-1998 (first entry)  
XX  
DE Light chain of a human antibody.  
XX  
KW Light chain; human; humanised immunoglobulin; NOK2; Fas ligand;  
KW inhibition; apoptosis; Fas expression; treatment; AIDS; rejection;  
KW transplant surgery; autoimmune disease; SLE; RA; diabetes.  
XX  
XX Homo sapiens.  
XX  
XX WO9810070-A1.  
XX  
XX 12-MAR-1998.  
XX  
XX 27-AUG-1997; 97WO-JP002983.  
XX  
XX 02-SEP-1996; 96JP-00231742.  
PR 20-SEP-1996; 96JP-00271546.  
XX  
XX (SUME) SUMITOMO ELECTRIC IND CO.  
XX  
XX Okumura K, Nakata M, Higuchi H, Ushio Y, Maeda H, Eda Y;  
XX WPI: 1998-193620/17.  
XX  
XX Human immunoglobulin or its active fragment specific for Fas ligand - for treatment of AIDS, organ rejection, autoimmune diseases e.g. systemic lupus erythematosus and diabetes.  
XX  
XX Disclosure; Page 261; 348pp; Japanese.  
XX  
XX The present sequence represents the light chain of a human antibody, and can be used in the humanised immunoglobulin of the invention. The humanised immunoglobulin reacts specifically with a region of a Fas ligand that is important in inhibiting apoptosis induced by cells with Fas expression. The immunoglobulin of the invention can inhibit physiological reactions between a Fas ligand and Fas, typified by apoptosis. The humanised immunoglobulin is used for treatment of AIDS, rejection following transplant surgery, autoimmune diseases such as SLE or RA, and diabetes  
XX  
XX Sequence 112 AA;  
Query Match 94.2%; Score 550; DB 2; Length 112;  
Best Local Similarity 93.8%; Pred. No. 2.3e-37;  
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DIVMTQSPISLPVTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60

Db 1 DIVMTQSLPLPVTTPGEPASISCRSSQSLHNSGYNLDWYLOKPGQSPQLLIYLSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQOS-PITFGQGTTRLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQLTPTVFGQGTTRLEIK 112

RESULT 13

ID ADI22126  
XX ADI22126 standard; protein; 113 AA.  
AC ADI22126;  
DT 22-APR-2004 (first entry)  
XX  
DE Anti-platelet autoantibody related light chain amino acid I50 SEQ.89.  
XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;  
KW thrombus; platelet adhesion inhibition;  
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;  
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;  
KW thrombolytic; human.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FN WO2004005890-A2.  
XX  
PD 15-JAN-2004.  
XX  
PF 03-JUL-2003; 2003WO-US021304.  
XX  
PR 03-JUL-2002; 2002US-0394352P.  
PR 18-SEP-2002; 2002US-0411694P.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
DR WPI; 2004-142998/14.  
DR N-PSDB; ADI22073.  
XX

PS Claim 12; SEQ ID NO 89; 232pp; English.

XX The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIB/IIIA, where the autoantibody, or its fragment comprises an antigen binding region derived from an H44L4 anti-platelet autoantibody, the kit further comprising a peptide

CC inhibitor of the binding with glycoprotein IIB/IIIA, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 113 AA;

Query Match 94.1%; Score 549.5; DB 8; Length 113;  
Best Local Similarity 94.7%; Pred. No. 2.6e-37;  
Matches 107; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 DIVMTQSLPLPVTTPGEPASISCRSSQSLHNSGYNLDWYLOKPGQSPQLLIYLSNRA 60  
Db 1 DIVMTQSLPLPVTTPGEPASISCRSSQSLHNSGYNLDWYLOKPGQSPQLLIYLSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQOS-PITFGQGTTRLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQLTPTVFGQGTTRLEIK 113

RESULT 14

ADJ76892  
ID ADJ76892 standard; protein; 112 AA.  
XX  
AC ADJ76892;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Anti-IGF-1R related protein #9.  
XX  
XX cytostatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX  
XX Homo sapiens.  
XX  
FN WO2003059951-A2.  
XX  
PD 24-JUL-2003.  
XX  
PF 20-JAN-2003; 2003WO-FR000178.  
XX  
PR 18-JAN-2002; 2002FR-00000653.  
PR 18-JAN-2002; 2002FR-00000654.  
PR 07-MAY-2002; 2002FR-00005753.  
XX  
PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
PI Goetsch L, Corvaia N, Leger O;  
XX  
DR WPI; 2003-569653/53.  
XX  
PT New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.  
XX  
PS Disclosure; SEQ ID NO 58; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit

CC transformation of normal cells to tumor cells, inhibit growth and/or  
CC proliferation of tumor cells, so are useful against cancers of the  
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 112 AA;

Query Match 93.8%; Score 548; DB 7; Length 112;  
Best Local Similarity 93.8%; Pred. No. 3.4e-37;  
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DIWMTQSPVLSPLVTPGEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60  
|||  
DB 1 DIWMTQSPVLSPLVTPGEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60  
|||  
QY 61 SGVPDRFSGSGGTDFTLKISRVEADGVVYCMQAQSPITFGQGLRLIK 112  
|||  
DB 61 SGVPDRFSGSGGTDFTLKISRVEADGVVYCMQAQSPITFGQGLRLIK 112  
|||

#### RESULT 15

AD122128  
ID AD122128 standard; protein; 112 AA.

XX AC AD122128;

XX DT 22-APR-2004 (first entry)

XX DE Anti-platelet autoantibody related light chain amino acid L52 SEQ:91.  
XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;  
XX thrombus; platelet adhesion inhibition;  
XX thrombotic thrombocytopenic purpura; platelet aggregation inhibition;  
XX idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;  
XX thrombolytic; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004005890-A2.

XX PD 15-JAN-2004.

XX XX 03-JUL-2003; 2003WO-US021304.

XX XX 03-JUL-2002; 2002US-0394352P.

XX PR 18-SEP-2002; 2002US-0411694P.

XX XX (UYPE-) UNIV PENNSYLVANIA.

XX XX Siegel DL;

XX XX WPI; 2004-142998/14.

XX DR N-PSDB; AD122075.

XX XX Claim 12; SEQ ID NO 91; 232pp; English.

XX The present invention describes a method (M1) for identifying an anti-  
XX platelet autoantibody (I) in a mammal. The autoantibody is detected by  
XX producing an antibody phage display library from B-lymphocytes obtained  
XX from the mammal, and screening the library to detect a phage that  
XX specifically binds with a platelet component, where the screening  
XX comprises panning the phage on intact platelets using competitive cell-  
XX surface panning. Also described: (1) an autoantibody identified by (M1);  
XX (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3)  
XX inhibiting (M2) blood clotting in a mammal having a thrombus or at risk  
XX of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a  
XX mammal having a thrombus or at risk of thrombus formation; (5) inhibiting  
XX (M4) binding of an anti-platelet autoantibody with a platelet component;  
XX (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6)  
XX thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)

CC platelet aggregation; (9) inhibiting (M8) platelet activation; (10)  
CC inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an  
CC anti-platelet autoantibody, or its biologically active fragment with a  
CC platelet; (12) identifying (M11) a peptide that inhibits binding of an  
CC anti-platelet autoantibody with a platelet; (13) a peptide identified by  
CC the method of (12); (14) a peptide that specifically binds with an anti-  
CC platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic  
CC purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood  
CC clotting, inhibiting platelet aggregation, inhibiting platelet function  
CC or inhibiting platelet activation comprising an amount of an anti-  
CC platelet autoantibody, or its biologically active fragment that  
CC specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or  
CC its fragment comprises an antigen binding region derived from an H44L4  
CC anti-platelet autoantibody, the kit further comprising a peptide  
CC inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator  
CC and an instructions for use. (I) has haemostatic, anticoagulant and  
CC thrombolytic activities. The autoantibodies (I) are useful for diagnosing  
CC and for developing therapeutics for diseases mediated by autoantibody  
CC binding with platelet antigens. (M6) and (M12) are useful for treating  
CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic  
CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood  
CC clotting. The present sequence is used in the exemplification of the  
XX present invention.

XX SQ Sequence 112 AA;

Query Match 93.8%; Score 548; DB 8; Length 112;

Best Local Similarity 93.8%; Pred. No. 3.4e-37;

Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIWMTQSPVLSPLVTPGEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60  
|||

DB 1 DIWMTQSPVLSPLVTPGEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLGSNRA 60  
|||

QY 61 SGVPDRFSGSGGTDFTLKISRVEADGVVYCMQAQSPITFGQGLRLIK 112  
|||

DB 61 SGVPDRFSGSGGTDFTLKISRVEADGVVYCMQAQSPITFGQGLRLIK 112  
|||

Search completed: November 16, 2005, 21:51:35

Job time : 66.2353 secs

(CASE) XIN/TO FOTD SHL

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 13.3824 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-2  
Perfect score: 584  
Sequence: 1 DIWVTOSPLSLPVTGPSPAS.....CMQAQSPITFGQGTREIK 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	93.8	112	2 S58207	Ig light chain V r
2	548	93.8	132	2 S26882	Ig kappa chain V r
3	548	93.8	135	2 S40342	Ig kappa chain - h
4	548	93.8	136	2 S40357	Ig kappa chain V-J
5	542	92.8	112	2 S58206	Ig light chain V r
6	536	91.8	117	1 K2HUGM	Ig kappa chain pre
7	536	91.8	125	2 S40356	Ig kappa chain - h
8	527.5	90.3	126	2 S40339	Ig kappa chain - h
9	525	89.9	113	1 K2HUTW	Ig kappa chain V-I
10	517	88.5	121	2 S40371	Ig kappa chain - h
11	514	88.0	131	2 S40372	Ig kappa chain V-J
12	499.5	85.5	112	1 K2HUMH	Ig kappa chain V-I
13	497.5	85.2	123	2 S40319	Ig kappa chain - h
14	488	83.6	100	2 S24681	Ig kappa chain - h
15	487	83.4	124	2 S03876	Ig kappa chain V-I
16	474.5	81.2	114	2 S40375	Ig kappa chain - h
17	471.5	80.7	130	2 S40321	Ig kappa chain - h
18	469	80.3	113	1 K2HUPR	Ig kappa chain V-I
19	464.5	79.5	115	1 K2HUCM	Ig kappa chain V-I
20	459.5	78.7	140	2 S22658	Ig kappa chain pre
21	458	78.4	142	2 S22902	Ig kappa chain V r
22	454	77.7	112	2 S38719	Ig light chain V r
23	454	77.7	112	2 F27887	Ig kappa chain V r
24	453	77.6	113	2 PL0203	anti-DNA autoantib
25	453	77.6	126	2 S40312	Ig kappa chain - h
26	452	77.4	131	2 B39276	Ig light chain pre
27	452	77.4	133	2 S23230	Ig kappa chain pre
28	452	77.4	219	2 S52028	Ig kappa chain - m
29	449.5	77.0	114	2 S40340	Ig kappa chain V-J

RESULT 1

S58207  
Ig light chain V region anti-F(ab')2 - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1996 #sequence\_revision 19-Apr-1996 #text\_change 21-Jan-2000  
C;Accession: S58207  
R;Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebl, S.; Breitling, I.  
submitted to the EMBL Data Library, July 1995  
A;Description: Characterization of heavy and light chain immunoglobulin variable region  
A;Reference number: S58206

A;Accession: S58207  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <WEL>  
A;Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;Keywords: immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 93.8%; Score 548; DB 2; Length 112;  
Best Local Similarity 93.8%; Pred.No. 4.5e-42;  
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIWVTOSPLSLPVTGPSPASISCRSSQSLHSGNYLDWYLOKPGOSPILLIYLGSNRA 60  
Db 1 DIWVTOSPLSLPVTGPSPASISCRSSQSLHSGNYLDWYLOKPGOSPILLIYLGSNRA 60  
Qy 61 SGVPDRPFGSGSGTDFTLKISRVEAEDGVYVCMAQOQSPITFGQGTREIK 112  
Db 61 SGVPDRPFGSGSGTDFTLKISRVEAEDGVYVCMAQOQSPITFGQGTREIK 112

RESULT 2

S26882  
Ig kappa chain V region (V607) - human

C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
C;Accession: S26882  
R;Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combratio, G.; Zachau, H.G.  
Nature 347, 90-92, 1990  
A;Title: Megabase inversions in the human genome as physiological events.  
A;Reference number: S26882; MUID:90370099; PMID:2118596

A;Accession: S26882  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-132 <WEI>  
A;Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367  
C;Genetics:  
A;Introns: 17/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;36-115/Domain: immunoglobulin homology <IMM>

ALIGNMENTS

Query Match 93.8%; Score 548; DB 2; Length 132;  
Best Local Similarity 93.8%; Pred. No. 5.3e-42; Indels 0; Gaps 0;  
Matches 105; Conservative 3; Mismatches 4;

Qy 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 21 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 80

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112  
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 132

RESULT 3  
S40342  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C:Accession: S40342  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40342  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-135 <KLE>  
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X72452; NID:G441372; PID:G441373  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 93.8%; Score 548; DB 2; Length 135;  
Best Local Similarity 93.8%; Pred. No. 5.5e-42; Indels 0; Gaps 0;  
Matches 105; Conservative 3; Mismatches 4;

Qy 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 14 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 73

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112  
Db 74 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 125

RESULT 4  
S40357  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C:Accession: S40357  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40357  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-136 <KLE>  
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X72467  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 93.8%; Score 548; DB 2; Length 136;  
Best Local Similarity 93.8%; Pred. No. 5.5e-42; Indels 0; Gaps 0;  
Matches 105; Conservative 3; Mismatches 4;

Qy 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 21 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 80

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112  
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 132

RESULT 5  
S58206  
Ig light chain V region anti-F(ab')2 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000  
C:Accession: S58206  
R:Weischof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, I.  
submitted to the EMBL Data Library, July 1995  
A:Description: Characterization of heavy and light chain immunoglobulin variable region  
A:Reference number: S58206  
A:Accession: S58206  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEL>  
A:Cross-references: EMBL:X89054; NID:G929640; PIDN:CAA61441.1; PID:G929641  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 542; DB 2; Length 112;  
Best Local Similarity 92.0%; Pred. No. 1.5e-41; Indels 0; Gaps 0;  
Matches 103; Conservative 4; Mismatches 5;

Qy 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGRLEIK 112

RESULT 6  
K2HUGM  
Ig kappa chain precursor V-II region (GM607) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
C:Accession: A01889; B24452  
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.  
Nature 309, 73-76, 1984  
A:Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.  
A:Reference number: A01889; MUID:84191506; PMID:6325927  
A:Accession: A01889  
A:Molecule type: mRNA  
A:Residues: 1-117 <KLO>  
A:Cross-references: UNIPROT:P06309  
A:Note: the sequence was determined from the differentiated gene  
C:Genetics:  
A:Gene: GDB:IGKV2  
A:Cross-references: GDB:I36265  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la;  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>  
F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>  
F:20-99/Domain: immunoglobulin homology <IMM>  
F:27-97/Disulfide bonds: #status predicted

Query Match 91.8%; Score 536; DB 1; Length 117;  
Best Local Similarity 92.0%; Pred. No. 5.5e-41; Indels 0; Gaps 0;  
Matches 103; Conservative 3; Mismatches 6;

Qy 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 5 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPHLLIYLGSNRA 64



```
QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQAQSQSPITFGQTRLEIK 112
|||||
Db 65 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQGLQTPQTFGQTKVEIK 116
|||||

RESULT 7
S40356
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40356
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40356
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72466; NID:G441400; PIDN:CAA51134.1; PID:G441401
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-104/Domain: immunoglobulin homology <IMM>

Query Match 91.8%; Score 536; DB 2; Length 125;
Best Local Similarity 91.1%; Pred. No. 5.9e-41;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRSGNYLDWYKQPSPLLIYLSNRA 60
|||||
Db 10 DIVMTQSPSLPVTGPEPASISCRSSQSLRHNGNYLDWYKQPSQLLIYLSNRA 69
|||||

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQAQSQSPITFGQTRLEIK 112
|||||
Db 70 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQVLIPLTFGGTKVEIK 121
|||||

RESULT 8
S40339
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40339
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40339
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-126 <KLE>
A:Cross-references: EMBL:X72449; NID:G441366; PIDN:CAA51117.1; PID:G441367
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-110/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 527.5; DB 2; Length 126;
Best Local Similarity 92.0%; Pred. No. 3.4e-40;
Matches 103; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRSGNYLDWYKQPSPLLIYLSNRA 60
|||||
Db 16 DIVMTQSPSLPVTGPEPASISCRSSQSLRHNGNYLDWYKQPSQLLIYLSNRA 75
|||||

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQAQSQSPITFGQTRLEIK 112
|||||
Db 76 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQ-PWTFGQTKVEIK 126
|||||

RESULT 9
K2HUTW
Ig kappa chain V-II region (Tew) - human (tentative sequence)
C:Species: Homo sapiens (man)
```

```
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A90370; A92764; A01888
R:Putnam, F.W.; Whitley Jr., E.J.; Paul, C.; Davidson, J.N.
Biochemistry 12, 3763-3780, 1973
A:Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloid
A:Reference number: A90370; MUID:74148480; PMID:4596149
A:Contents: Bence Jones protein Tew
A:Accession: A90370
A:Molecule type: protein
A:Residues: 1-113 <PUT>
A:Cross-references: UNIPROT:P01617
A>Note: this protein was isolated from the urine of a patient with plasma cell dyscrasia;
A>Note: the C region of this chain has the Inv (1,2) marker
R:Terrey, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osseman, E.F.; Glenner, G.G.
J. Clin. Invest. 52, 1276-1281, 1973
A:Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient with
A:Reference number: A92764; MUID:73166638; PMID:4700495
A:Contents: amyloid protein Tew
A:Accession: A92764
A:Molecule type: protein
A:Residues: 1-27 <TER>
A>Note: the major amyloid protein appears to be identical with the Bence Jones protein in
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la;
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 89.9%; Score 525; DB 1; Length 113;
Best Local Similarity 90.2%; Pred. No. 5.1e-40;
Matches 101; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRSGNYLDWYKQPSPLLIYLSNRA 60
|||||
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRHSDGFDYLNWYKQPSPLLIYLSNRA 60
|||||

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQAQSQSPITFGQTRLEIK 112
|||||
Db 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMZALQAPITFGQTRLEIK 112
|||||

RESULT 10
S40371
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40371
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40371
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <KLE>
A:Cross-references: EMBL:X72481; NID:G441430; PIDN:CAA51149.1; PID:G441431
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 517; DB 2; Length 121;
Best Local Similarity 90.8%; Pred. No. 2.8e-39;
Matches 99; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 MTQSPSLPVTGPEPASISCRSSQSLRSGNYLDWYKQPSPLLIYLSNRA 63
|||||
Db 1 MTQSPSLPVTGPEPASISCRSSQSLRYSTGYNDWYKQPSQLLIYLSKRASGV 60
|||||
```

**Qy** 64 PDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQQSPITFGQGTRLEIK 112  
|||  
**Db** 61 PDRFSGSGSGTDFTLKISRVEAEDGVVYCMQGLTOTPTTFGQGTKLEIK 109  
|||

## RESULT 11

Ig kappa chain V-J region - human  
 C;Species: Homo sapiens (man)  
 C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C;Accession: S40372  
 R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A;Reference number: S40312; MUID: 94080891; PMID: 8258341  
 A;Accession: S40372  
 A;Status: preliminary; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-131 <KLE>  
 A;Cross-references: EMBL:X72482; NID:g441432; PIDN:CAAS1150.1; PID:g441433  
 C;Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F:36-115/Domain: immunoglobulin homology <IMM>

Query Match	88.0%	Score 514;	DB 2;	Length 131;
Best Local Similarity	88.3%	Pred. No. 5.7e-39;		
Matches	98;	Mismatches	8;	Gaps
Conservative				

<b>Qy</b>	1	DIVMTQSP	LSPVTPGEPASISCRSSQSLLRSGNYL	LDWYLPKPGQSPHLLIYLGSNRA	60
			:         :		
<b>Dd</b>	21	DIVMTQSP	LSPVTPGESA	SFSECKTSOSLLHNGHNHYL	80

Qy		61	SGVPDFSSGSGTDFTLKISRVEADVGYYVCMQAQQSPITFGQGTRLEI	111
			:	
p <sub>b</sub>		81	SGVPDFSSGSGSGTDFTLKISRVEADVGYYVCMQPLOTPTTFGGQTKEI	131

## RESULT 12

K2HUM1  
Ig kappa chain V-II region (Mil) - human (tentative sequence)  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C:Accession: A01887  
R:Dreyer, W.J.; Gray, W.R.; Hood, L.  
Cold Spring Harb. Symp. Quant. Biol. 32, 353-367, 1967  
A:Title: The genetic, molecular, and cellular basis of antibody formation: some facts and  
A:Reference number: A01887  
A:Accession: A01887  
A:Molecule type: protein  
A:Residues: 1-112 <DRE>  
A:Cross-references: UNIPROT:P01616  
A:Note: the C region of this chain has the Inv (3) marker  
C:Comment: This is a Bence Jones protein.

A: Gene: GDB: IGVK2  
A: Cross-references: GDB: I36265  
A: Map position: 2p12-2p12  
C: Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associated with the heavy chain form a heterodimer with two identical heavy chain disulfide bonds.  
C: Superfamily: immunoglobulin V region; immunoglobulin homology  
C: Keywords: heterotetramer  
F: 16-94/Domain: immunoglobulin homology <IMM>  
F: 23-92/Disulfide bonds: #status predicted

Query Match	85.5%;	Score	499.5;	DB 1;	Length	112;			
Best Local Similarity	82.1%;	Pred. No.	9.5e-38;						
Matches	92;	Conservative	14;	Mismatches	5;	Indels	11;	Gaps	1;

[illegible]61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMOAQSPITFGGTRLEIK 112  
Ov

Db 60 SGVPRFSGSGTBFILKISRVAZBVGYYCMQALOTPLTFGGTNV EIK 111

## RESULT 13

Ig kappa chain V region - human  
 C;Species: Homo sapiens (man)  
 C;Date: 19-May-1994 #sequence 26-May-1995 #text\_change 21-Jan-2000  
 C;Accession: S40319  
 R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A;Reference number: S40312; MUID:94080891; PMID:8258341  
 A;Accession: S40319  
 A;Status: preliminary; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-123 <KLE>  
 A;Cross-references: EMBL:X72429; NID:g441326; PIDN:CAA51097.1; PID:g441327  
 C;Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F:26-105/Domain: immunoglobulin homology <IMM>

Query Match	85.2%	Score 497.5;	DB 2;	Length 123;
Best Local Similarity	89.7%;	Pred. No. 1.6e-37;		
Matches	96;	Conservative	5;	Mismatches 5;
				Indels 1;
				Gaps 1;

<b>QY</b>	1	DIVMTQSPLSLPVTGPGEPAISCRSSQSLFRSNGYNVLDWYLKPGQSPHLLIYLGSNRA	60
		:	:
<b>pB</b>	11	DIVMTQSPLSLPVTGPGEPAISCRSSQSLFRSNGYDVLWDYKPGQSPOLLIYLGSNRA	70

**QY** 61 SGVPDRFSGSGTDFTLKISRVEAEDGVYYCMQAQQSP-ITFGQG 106  
|||||  
||||| : ||

**nB** 71 SGVPDRFSGSGTDFTLKISRVEAEDGVYYCMQAALOTPSVTSAGK 117  
|||||  
||||| :

DEFINITION 14

S24681  
Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S24681  
R;van Es, J.H.  
submitted to the EMBL Data Library, July 1992  
A;Reference number: S24679  
A;Accession: S24681  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-100 <VAN>  
A;Cross-references: EMBL:X67904; NID:G33435; PID:CAA48102.1; PID:G33436  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match	83.6%	Score 488;	DB 2;	Length 100;
Best Local Similarity	94.0%	Pred. No. 8.9e-37;		
Matches q4. Conservative	1:	Mismatches 5;	Indels 0;	Gaps 0;

Qy	1	DIVMTQSPISLPVTTPGEPAISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA	60
Ph	1	DIVMTQSPISLPVTTPGEPAISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA	60

Qy 61 SGVPDRFSCSGSTDFTLKISRVEADVGVYYCMQAQSP 100  
|||||  
nb 61 SGVDRPFSCSGSTDFTLKISRVEADVGVYYCMQAQSP 100  
|||||

LEADER

S03876  
Ig kappa chain V-II region (Inc) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C:Accession: S03876

R:Perri, G.; Stoppini, M.; Iadarola, P.; Bellotti, V.; Merlini, G.  
 Biochim. Biophys. Acta 995, 103-108, 1989  
 A:Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.  
 A:Reference number: S03876; MUID:89194238; PMID:2495028  
 A:Accession: S03876  
 A:Molecule type: protein  
 A:Residues: 1-124 <PER>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 487; DB 2; Length 124;  
 Best Local Similarity 83.0%; Pred. No. 1.4e-36;  
 Matches 93; Conservative 9; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 DIVMTQSPLEVTPEGPASISCRSSQSLRRNGNYLDWYLQKPGQSPHLLIYLGSNRA 60  
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 DIVLTQSPLEVTPEGPASISCKSSQSLMHSSGDNLYLDWYLQKPGQSPQIVILGYNRA 60  
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 SGVPRFSGSGGTDFTLKISRVEADGVYYCMQAQSPITFGQSTRLEIK 112  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 61 SGVPTDFSGSGGTDFTLISSVGAEDGVYYCMQALQPTWTFGQTKVGIK 112  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: November 16, 2005, 22:04:06  
 Job time : 14.3824 secs

THE NEW YORK PUBLIC LIBRARY  
ASTOR LENOX TILDEN FOUNDATION  
1911

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 62.7941 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-2  
Perfect score: 584  
Sequence: 1 DIVMTQSLSLPVTGEPAS.....CMQAQSPITFGQTRLEIK 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	536	91.8	117	1	KV2E_HUMAN	P06309 homo sapien
2	535	91.6	239	2	Q8NEK0	Q8NEK0 homo sapien
3	525	89.9	113	1	KV2D_HUMAN	P01617 homo sapien
4	519.5	89.0	240	2	Q6PIH6	Q6PIH6 homo sapien
5	499.5	85.5	112	1	KV2C_HUMAN	P01616 homo sapien
6	469	80.3	113	1	KV2B_HUMAN	P01615 homo sapien
7	464.5	79.5	115	1	KV2A_HUMAN	P01614 homo sapien
8	450	77.1	248	2	Q65ZQ7	Q65ZQ7 mus sp. b3(
9	447	76.5	239	2	Q6P491	Q6P491 homo sapien
10	446	76.4	239	2	Q8TCD0	Q8TCD0 homo sapien
11	444	76.0	133	1	KV2F_HUMAN	P06310 homo sapien
12	437	74.8	113	1	KV2G_MOUSE	P01631 mus musculus
13	428.5	73.4	114	2	Q9UL80	Q9UL80 homo sapien
14	428	73.3	219	2	Q65ZC0	Q65ZC0 mus musculus
15	420	71.9	113	1	KV2F_MOUSE	P01630 mus musculus
16	418	71.6	112	1	KV2D_MOUSE	P01629 mus musculus
17	416	71.2	113	1	KV2E_MOUSE	P01976 mus musculus
18	415.5	71.1	108	1	KV1_CANFA	P01618 canis famill
19	405	69.3	112	2	Q6LEM8	Q6LEM8 mus musculus
20	405	69.3	113	1	KV2C_MOUSE	P01628 mus musculus
21	399	68.3	112	1	KV2A_MOUSE	P01626 mus musculus
22	389.5	66.7	114	1	KV4A_HUMAN	P01625 homo sapien
23	381.5	65.3	134	1	KV4C_HUMAN	P06314 homo sapien
24	378.5	64.8	255	2	Q6K805	Q6K805 mus musculus
25	374	64.0	109	1	KV3D_HUMAN	P01622 homo sapien
26	372	63.7	129	1	KV3L_HUMAN	P18135 homo sapien
27	371	63.5	109	2	Q9UL78	Q9UL78 homo sapien
28	371	63.5	133	1	KV4B_HUMAN	P06313 homo sapien
29	369	63.2	120	1	KV2B_MOUSE	P01627 mus musculus
30	367	62.8	109	1	KV3E_HUMAN	P01620 homo sapien
31	367	62.8	129	1	KV3M_HUMAN	P18136 homo sapien

32	365.5	62.6	111	1	KV3S_MOUSE	P01671 mus musculus
33	365.5	62.6	236	2	Q6PIL8	Q6PIL8 homo sapien
34	364.5	62.4	111	1	KV3U_MOUSE	P01673 mus musculus
35	364	62.3	108	1	KV3A_HUMAN	P01619 homo sapien
36	363.5	62.2	111	2	Q920E9	Q920E9 mus musculus
37	363.5	61.9	111	1	KV3R_MOUSE	P01670 mus musculus
38	359	61.5	109	1	KV3E_HUMAN	P01623 homo sapien
39	359	61.5	109	1	KV3G_HUMAN	P04206 homo sapien
40	358	61.3	235	2	Q6GMV9	Q6GMV9 homo sapien
41	355.5	60.9	111	1	KV3M_MOUSE	P01665 mus musculus
42	354.5	60.7	111	1	KV3N_MOUSE	P01666 mus musculus
43	354.5	60.7	111	1	KV3T_MOUSE	P01672 mus musculus
44	354	60.6	109	1	KV3F_HUMAN	P01624 homo sapien
45	353.5	60.5	109	1	KV4D_HUMAN	P83593 homo sapien

ALIGNMENTS

RESULT 1  
KV2E\_HUMAN  
ID KV2E\_HUMAN STANDARD; PRT; 117 AA.  
AC P06309;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region GM607 precursor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBP\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84191506; PubMed=6325927;  
RA Klobeck H.G., Solomon A., Zachau H.G.;  
RT "Contribution of human V kappa II germ-line genes to light-chain  
RT diversity";  
RL Nature 309:73-76(1984).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; 200009; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A01889; K2HUGM.  
DR HSSP; Q99M37; 1191.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT NON\_TER 1 1  
FT SIGNAL <1 4  
FT CHAIN 5 117 Ig kappa chain V-II region GM607.  
FT DOMAIN 5 27 Framework-1.  
FT DOMAIN 28 43 Complementarity-determining-1.  
FT DOMAIN 44 58 Framework-2.  
FT DOMAIN 59 65 Complementarity-determining-2.  
FT DOMAIN 66 97 Framework-3.  
FT DOMAIN 98 106 Complementarity-determining-3.  
FT DOMAIN 107 116 Framework-4.  
FT DISULFID 27 97 By similarity.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E559B1 CRC64;

Query Match 91.8%; Score 536; DB 1; Length 117;  
 Best Local Similarity 92.0%; Pred. No. 5.1e-48;  
 Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 DIVMTOSPLSLPVTGPPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 60  
 DB 5 DIVMTOSPLSLPVTGPPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 64  
 QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYCMQAQSQSPITPGQGTREIK 112  
 DB 65 SGVPDRFSGSGGTDFTLKISRVEADVGYYCMQAQSQSPITPGQGTREIK 116

RESULT 2  
 Q8NEKO PRELIMINARY; PRT; 239 AA.  
 AC Q8NEKO;  
 DT 01-OCT-2002 (T-REMBLrel. 22, Created)  
 DT 01-OCT-2002 (T-REMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (T-REMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Tkatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Tapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Strauberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC030814; AA030814.1; -.  
 DR PIR: S23638; S23638.  
 DR PIR: S34091; S34091.  
 DR PIR: S40342; S40342.  
 DR PIR: S40357; S40357.  
 DR HSP: P01834; I17Z.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; Cl-set; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS0835; IG LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC;  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;

Matches 101; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DIVMTOSPLSLPVTGPPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 60  
 DB 21 DIVMTOSPLSLPVTGPPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 80  
 QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYCMQAQSQSPITPGQGTREIK 112  
 DB 81 SGVPDRFSGSGGTDFTLKISRVEADVGYYCMQAQSQSPITPGQGTREIK 132

RESULT 3  
 KV2D HUMAN STANDARD; PRT; 113 AA.  
 AC P016I7;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-II region TEW.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE (BENCE-JONES PROTEIN TEW).  
 RX MEDLINE=74148480; PubMed=4596149;  
 RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;  
 RT "Amino acid sequence of a kappa Bence Jones protein from a case of  
 primary amyloidosis.";  
 RL Biochemistry 12:3763-3780(1973).  
 RN [2]  
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).  
 RX MEDLINE=73166638; PubMed=4700495;  
 RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,  
 RA Glenner G.G.;  
 RT "Structural identity of Bence Jones and amyloid fibril proteins in a  
 patient with plasma cell dyscrasia and amyloidosis.";  
 RL J. Clin. Invest. 52:1276-1281(1973).  
 CC -1- MISCELLANEOUS: The major amyloid protein appears to be identical  
 with the Bence Jones protein isolated from the same patient.  
 CC -1- MISCELLANEOUS: This protein was isolated from the urine of a  
 patient with plasma cell dyscrasia and amyloidosis.  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
 marker.  
 DR PIR: A90370; K2HUTW.  
 DR HSP: Q99M37; I191.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS0835; IG LIKE; 1.  
 DR Anlyoid; Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 39 Complementarity-determining-1.  
 FT DOMAIN 40 54 Framework-2.  
 FT DOMAIN 55 61 Complementarity-determining-2.  
 FT DOMAIN 62 93 Framework-3.  
 FT DOMAIN 94 102 Complementarity-determining-3.  
 FT DOMAIN 103 112 Framework-4.  
 FT DISULFID 23 93 By similarity.  
 FT NON TER 113 113  
 SQ SEQUENCE 113 AA; 0C3C38F81F1843CA CRC64;

Query Match 89.9%; Score 525; DB 1; Length 113;  
 Best Local Similarity 90.2%; Pred. No. 6.9e-47;  
 Matches 101; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DIVMTOSPLSLPVTGPPEPASISCRSSQSLRSGNYLDWYLOKPGQSPHLLIYLSNRA 60

```
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSDGDFLWYLNWYLOKPGQSPZLLIYLSNRA 60
QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQAQQSPITFGQGTTRLEIK 112
Db 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMZALQAPITFGQGTTRLEIK 112

RESULT 4
Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K.B., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; -
DR HSSP; P01837; 1KB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188B4DB8B781EC4 CRC64;

Query Match 89.0%; Score 519.5; DB 2; Length 240;
Best Local Similarity 90.3%; Pred. No. 6.3e-46;
Matches 102; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSDGDFLWYLNWYLOKPGQSPZLLIYLSNRA 60
Db 21 DIVMAQSPSLSVTGPPEPASISCRSSQSLHSDGDFLWYLNWYLOKPGQSPZLLIYLSNRA 80
QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQAQQSPITFGQGTTRLEIK 112
```

```
Db 81 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQAQQSPITFGQGTTRLEIK 133

RESULT 5
KV2C_HUMAN STANDARD; PRT; 112 AA.
ID KV2C_HUMAN
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis."
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367 (1967).
CC -!- MISCELLANEOUS; The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS; This is a Bence-Jones protein.
DR PIR; A01887; K2HUML.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 85.5%; Score 499.5; DB 1; Length 112;
Best Local Similarity 82.1%; Pred. No. 3.1e-44;
Matches 92; Conservative 14; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSDGDFLWYLNWYLOKPGQSPZLLIYLSNRA 60
Db 1 DIVLQSPSLPVTGPPEPASISCRSSQSLHSDGDFLWYLNWYLOKPGQSPZLLIYLSNRA 59
QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQAQQSPITFGQGTTRLEIK 112
Db 60 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQAQQSPITFGGTVNEIK 111

RESULT 6
KV2B_HUMAN STANDARD; PRT; 113 AA.
ID KV2B_HUMAN
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riessen W.F., Jatton J.-C.;
```





DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX SEQUENCE FROM N.A.  
 RP TISSUE=Skin;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC063599; AAH63599.1; -  
 DR HSSP; P01837; IKCU.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;  
 Query Match 76.5%; Score 447; DB 2; Length 239;  
 Best Local Similarity 78.6%; Pred. No. 2.3e-38;  
 Matches 88; Conservative 6; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRLNGYNYLDWYKQKQSPHLLIYLGSNRA 60  
 DB 21 DIVMTQSPSLPVTGPEPASISCRSSQSLRLNGYNYLDWYKQKQSPHLLIYKISNRF 80  
 QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMAQSQSPITFGQGTREIK 112  
 DB 81 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMAQSQSPITFGQGTREIK 132  
 RESULT 10  
 Q8TCD0 PRELIMINARY; PRT; 239 AA.  
 AC Q8TCD0;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC022362; AAH22362.1; -  
 DR PIR; S22658; S22658.  
 DR PIR; S34095; S34095.  
 DR PIR; S40324; S40324.  
 DR PIR; S40374; S40374.  
 DR PIR; S42267; S42267.  
 DR PIR; S42268; S42268.  
 DR HSSP; P01834; 1172.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;  
 Query Match 76.4%; Score 446; DB 2; Length 239;  
 Best Local Similarity 76.8%; Pred. No. 2.9e-38;  
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLRLNGYNYLDWYKQKQSPHLLIYLGSNRA 60  
 DB 21 DIVMTQSPSLPVTGPEPASISCRSSQSLRLNGYNYLDWYKQKQSPHLLIYKISNRF 80  
 QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMAQSQSPITFGQGTREIK 112  
 DB 81 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMAQSQSPITFGQGTREIK 132  
 RESULT 11  
 KV2F HUMAN  
 ID KV2F HUMAN STANDARD; PRT; 133 AA.  
 AC P06310;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region RPMI 6410 precursor.  
 OS Homo sapiens (Human).





(0150) MAY 11 1961 SHL

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 19.0441 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357A-2  
Perfect score: 584  
Sequence: 1 DIVMTQSLPLVTPGEPAS.....CMQAQSPITFGGTRLEIK 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: +  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/PGTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	94.7	113	3	US-09-025-769B-15
2	553	94.7	113	4	US-09-490-070A-15
3	553	94.7	113	4	US-09-490-153-15
4	553	94.7	113	4	US-09-490-324-15
5	550	94.2	112	4	US-09-254-180C-9
6	536	91.8	112	1	US-08-331-398A-9
7	536	91.8	112	2	US-08-331-397B-49
8	536	91.8	112	2	US-08-759-804A-49
9	536	91.8	112	3	US-09-227-693-49
10	532	91.1	114	3	US-09-025-769B-29
11	532	91.1	114	3	US-09-025-769B-45
12	532	91.1	114	4	US-09-490-070A-29
13	532	91.1	114	4	US-09-490-070A-45
14	532	91.1	114	4	US-09-490-153-29
15	532	91.1	114	4	US-09-490-153-45
16	532	91.1	114	4	US-09-490-324-29
17	532	91.1	114	4	US-09-490-324-45
18	532	91.1	281	3	US-09-025-769B-178
19	532	91.1	281	4	US-09-490-070A-178
20	532	91.1	281	4	US-09-490-153-178
21	532	91.1	281	1	US-09-490-324-178
22	527	90.2	112	1	US-08-053-171-16
23	521	89.2	113	1	US-08-082-623-4
24	511	87.5	239	4	US-10-000-489-8
25	509	87.2	112	3	US-09-000-088-2
26	508	87.0	112	3	US-09-240-274-30
27	507	86.8	108	1	US-08-488-113B-151

Sequence 151, App  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 151, App  
Sequence 15, Appl  
Sequence 15, App  
Sequence 151, App  
Sequence 15, App  
Sequence 151, App  
Sequence 88, Appl  
Sequence 88, Appl  
Sequence 115, App  
Sequence 66, Appl  
Sequence 66, Appl  
Sequence 66, Appl  
Sequence 66, Appl  
Sequence 66, Appl

ALIGNMENTS

RESULT 1  
US-09-025-769B-15  
; Sequence 15, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Illeg, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: -Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-15

Query Match 94.7%; Score 553; DB 3; Length 113;  
Best Local Similarity 94.6%; Pred. No. 7.3e-47;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPGPASCSSQSLRLSNGVNYLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 1 DIVMTQSLPLPVTGPGPASCSSQSLRLSNGVNYLDWYLOKPGQSPHLLIYLGSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQSQSPITFGQGTREIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQSQSPITFGQGTREIK 112

RESULT 2  
US-09-490-070A-15  
; Sequence 15, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & McAuliffe  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-490-070A-15

Query Match 94.7%; Score 553; DB 4; Length 113;  
Best Local Similarity 94.6%; Pred. No. 7.3e-47;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 DIVMTQSLPLPVTGPGPASCSSQSLRLSNGVNYLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 1 DIVMTQSLPLPVTGPGPASCSSQSLRLSNGVNYLDWYLOKPGQSPHLLIYLGSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQSQSPITFGQGTREIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQSQSPITFGQGTREIK 112

RESULT 3

US-09-490-153-15  
; Sequence 15, Application US/09490153  
; Patent No. 6706484  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,153  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-490-153-15  
Query Match 94.7%; Score 553; DB 4; Length 113;  
Best Local Similarity 94.6%; Pred. No. 7.3e-47;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 DIVMTQSLPLPVTGPGPASCSSQSLRLSNGVNYLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 1 DIVMTQSLPLPVTGPGPASCSSQSLRLSNGVNYLDWYLOKPGQSPHLLIYLGSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQSQSPITFGQGTREIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQSQSPITFGQGTREIK 112  
RESULT 4  
US-09-490-324-15  
; Sequence 15, Application US/09490324  
; Patent No. 6828422  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas

;; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
;; NUMBER OF SEQUENCES: 373  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
;; STREET: 1251 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10021

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; FILING APPLICATION NUMBER: US/09/490,324  
;; FILING DATE: 24-Jan-2000

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/025,769  
;; FILING DATE: 18-FEB-1998  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090

;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 113 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear

;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-490-324-15

Query Match 94.7%; Score 553; DB 4; Length 113;  
Best Local Similarity 94.6%; Pred. No. 7.3e-47;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Db 1 DIVMTQSLPLVPTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

## RESULT 5

US-09-254-180C-9  
;; Sequence 9, Application US/09254180C  
;; Patent No. 6777540

;; GENERAL INFORMATION:

;; APPLICANT: OKUMURA, Ko

;; APPLICANT: EDA, Yasuyuki

;; APPLICANT: MAEDA, Hiroaki

;; APPLICANT: USHIO, Yoshitaka

;; APPLICANT: HIGUCHI, Hirofumi

;; APPLICANT: NAKATA, Motoni

;; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or  
;; INFORMATION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand

;; FILE REFERENCE: 050006-0055

;; CURRENT APPLICATION NUMBER: US/09/254,180C

;; CURRENT FILING DATE: 1999-04-15

;; PRIOR APPLICATION NUMBER: PCT/JP97/02983

;; PRIOR FILING DATE: 1997-08-27

;; PRIOR APPLICATION NUMBER: 271546/1996

;; PRIOR FILING DATE: 1996-09-20

;; PRIOR APPLICATION NUMBER: 231472/1996

;; PRIOR FILING DATE: 1996-09-02  
;; NUMBER OF SEQ ID NOS: 183  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 9  
;; LENGTH: 112  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-254-180C-9

Query Match 94.2%; Score 550; DB 4; Length 112;  
Best Local Similarity 93.8%; Pred. No. 1.4e-46;  
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Db 1 DIVMTQSLPLVPTGPEPASISCRSSQSLRLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

## RESULT 6

US-08-331-398A-49  
;; Sequence 49, Application US/08331398A  
;; Patent No. 5608039

;; GENERAL INFORMATION:

;; APPLICANT: Paetan, Ira

;; APPLICANT: Willingham, Mark

;; APPLICANT: Fitzgerald, David

;; APPLICANT: Brinkmann, Ulrich

;; APPLICANT: Pai, Lee

;; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
;; and Their Uses (as amended)

;; NUMBER OF SEQUENCES: 68

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew

;; STREET: One Market Plaza, Steuart Street Plaza

;; CITY: San Francisco

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94105-1492

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA: US/08/331,398A

;; APPLICATION NUMBER: US/08/331,398A

;; FILING DATE: 28-OCT-1994

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/767,331

;; FILING DATE: 30-SEP-1991

;; PRIOR APPLICATION DATA: US 07/596,289

;; APPLICATION NUMBER: US 07/596,289

;; FILING DATE: 12-OCT-1990

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hunter, Tom

;; REGISTRATION NUMBER: 38,498

;; REFERENCE/DOCKET NUMBER: 015280-126110US

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 543-9600

;; TELEFAX: (415) 543-5043

;; INFORMATION FOR SEQ ID NO: 49:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 112 amino acids

;; TYPE: amino acid

;; STRANDEDNESS:

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; FEATURE:

;; NAME/KEY: Protein





Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSPSLPVTGPSPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 1 DIVMTQSPSLPVTGPSPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112

RESULT 9  
US-09-227-693-49  
; Sequence 49, Application US/09227693  
; Patent No. 6287562  
; GENERAL INFORMATION:  
; APPLICANT: PASTAN, Ita  
; APPLICANT: BENHAR, Itai  
; APPLICANT: PADLAN, Eduardo A.  
; APPLICANT: JUNG, Sun-Hee  
; APPLICANT: LEE, Byungkook  
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY  
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/227,693  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/331,396  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 15280-136-1-3  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..112  
; OTHER INFORMATION: /note= "Human IgM GM607 VL region"

US-09-227-693-49  
Query Match 91.8%; Score 536; DB 3; Length 112;  
Best Local Similarity 92.08; Pred. No. 3.3e-45;  
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSPSLPVTGPSPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60

Db 1 DIVMTQSPSLPVTGPSPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112

RESULT 10  
US-09-025-769B-29  
; Sequence 29, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-29

Query Match 91.1%; Score 532; DB 3; Length 114;  
Best Local Similarity 91.1%; Pred. No. 8.4e-45;  
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSPSLPVTGPSPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60  
Db 1 DIVMTQSPSLPVTGPSPASISCRSSQSLHNSGYNLDWYLOKPGQSPHLLIYLGSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAGQSPITFGQGRLEIK 112

RESULT 11  
US-09-025-769B-45  
; Sequence 45, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 45:  
LENGTH: 114 amino acids  
TYPE: amino acid  
MOLECULE TYPE: protein  
TOPOLOGY: linear  
US-09-025-769B-45

Query Match 91.1%; Score 532; DB 3; Length 114;  
Best Local Similarity 91.1%; Pred. No. 8.4e-45;  
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60  
Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60

Qy 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVYCMQAQOQSPITFGQGRLEIK 112  
Db 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVYCMQAQOQSPITFGQGRLEIK 112

RESULT 12  
US-09-490-070A-29  
Sequence 29, Application US/09490070A  
Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.

COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-490-070A-29

Query Match 91.1%; Score 532; DB 4; Length 114;  
Best Local Similarity 91.1%; Pred. No. 8.4e-45;  
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60  
Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60

Qy 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVYCMQAQOQSPITFGQGRLEIK 112  
Db 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVYCMQAQOQSPITFGQGRLEIK 112

RESULT 13  
US-09-490-070A-45  
Sequence 45, Application US/09490070A  
Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:

```
;
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-070A-45

Query Match          91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60
DB 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRK 112
DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRK 112

RESULT 14
US-09-490-153-29
; Sequence 29, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-070A-45

Query Match          91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60
DB 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRK 112
DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRK 112

RESULT 14
US-09-490-153-29
; Sequence 29, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-070A-45
```

```
;
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-153-29

Query Match          91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60
DB 1 DIVMTQSLPLVPTPGEPASISCRSSQSLRSNGYNYLDWYLOKPGQSPHLLIYLSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRK 112
DB 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTRLRK 112

RESULT 15
US-09-490-153-45
; Sequence 45, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-153-45

Query Match          91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

Qy	1	DIVMTQSP	LSLPVT	PGEPAS	ISCRSS	QSL	LRNG	YNYL	DWY	LQK	PGQ	SPH	LLI	Y	L	G	S	N	R	A	60																									
Db	1	DIVMTQSP	LSLPVT	PGEPAS	ISCRSS	QSL	LRNG	YNYL	DWY	LQK	PGQ	SPH	LLI	Y	L	G	S	N	R	A	60																									
Qy	61	SGV	PD	R	F	S	G	S	G	T	D	F	T	L	K	I	S	R	V	E	A	E	D	V	G	V	Y	C	M	A	O	Q	S	P	I	T	F	G	Q	T	R	L	E	I	K	112
Db	61	SGV	PD	R	F	S	G	S	G	T	D	F	T	L	K	I	S	R	V	E	A	E	D	V	G	V	Y	C	M	A	O	Q	S	P	I	T	F	G	Q	T	R	L	E	I	K	112

Search completed: November 16, 2005, 22:07:17  
Job time : 19.0441 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 68.7647 Seconds  
(without alignments)  
681.481 Million cell updates/sec

Title: US-10-660-357A-2

Perfect score: 594

Sequence: 1 DIWVTSPLSLPTGPEPAS.....CMQAQSPITFGGTRLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	584	100.0	112	14	US-10-330-613-2
2	584	100.0	112	14	US-10-330-530-2
3	584	100.0	112	16	US-10-660-357-2
4	556	95.2	112	20	US-11-021-715-93
5	554	94.9	112	15	US-10-292-088-52
6	554	94.9	239	15	US-10-292-088-56
7	553	94.7	112	15	US-10-292-088-104
8	553	94.7	112	20	US-11-021-715-75
9	553	94.7	112	20	US-11-021-715-90
10	552	94.5	112	20	US-11-021-715-74
11	552	94.5	112	20	US-11-021-715-86
Sequence 2, Appli					
Sequence 2, Appli					
Sequence 2, Appli					
Sequence 93, Appli					
Sequence 52, Appli					
Sequence 56, Appli					
Sequence 104, Appli					
Sequence 75, Appli					
Sequence 90, Appli					
Sequence 74, Appli					
Sequence 86, Appli					

12	552	94.5	134	17	US-10-858-855-8	Sequence 8, Appli
13	551	94.3	112	20	US-11-021-715-87	Sequence 87, Appli
14	549.5	94.1	113	20	US-11-021-715-89	Sequence 89, Appli
15	548	93.8	112	15	US-10-292-088-103	Sequence 103, Appli
16	548	93.8	112	15	US-10-292-088-111	Sequence 111, Appli
17	548	93.8	112	17	US-10-877-773-30	Sequence 30, Appli
18	548	93.8	112	17	US-10-877-773-30	Sequence 30, Appli
19	548	93.8	112	17	US-10-735-918A-58	Sequence 58, Appli
20	548	93.8	112	20	US-11-021-715-91	Sequence 91, Appli
21	548	93.8	113	15	US-10-308-817-177	Sequence 177, Appli
22	548	93.8	113	15	US-10-453-698-177	Sequence 177, Appli
23	548	93.8	113	17	US-10-726-332-212	Sequence 212, Appli
24	548	93.8	125	14	US-10-010-942B-6	Sequence 6, Appli
25	548	93.8	125	15	US-10-388-383-6	Sequence 6, Appli
26	548	93.8	125	16	US-10-703-713-6	Sequence 6, Appli
27	548	93.8	125	16	US-10-704-070-6	Sequence 6, Appli
28	548	93.8	125	17	US-10-232-030-6	Sequence 18, Appli
29	546	93.5	112	14	US-10-269-805-18	Sequence 26, Appli
30	546	93.5	112	14	US-10-269-805-26	Sequence 26, Appli
31	546	93.5	112	15	US-10-309-762-33	Sequence 33, Appli
32	545.5	93.4	113	20	US-11-021-715-88	Sequence 63, Appli
33	545	93.3	112	16	US-10-663-244-63	Sequence 63, Appli
34	545	93.3	112	20	US-11-021-715-77	Sequence 77, Appli
35	545	93.3	112	20	US-11-021-715-81	Sequence 81, Appli
36	545	93.3	112	20	US-11-021-715-92	Sequence 92, Appli
37	545	93.3	238	16	US-10-663-244-145	Sequence 145, Appli
38	544.5	93.2	112	20	US-11-031-485-123	Sequence 123, Appli
39	544.5	93.2	238	20	US-11-031-485-4	Sequence 4, Appli
40	544	93.2	112	20	US-11-021-715-82	Sequence 82, Appli
41	543.5	93.1	112	17	US-10-726-332-215	Sequence 215, Appli
42	542	92.8	112	15	US-10-292-088-12	Sequence 12, Appli
43	542	92.8	112	15	US-10-292-088-28	Sequence 28, Appli
44	542	92.8	112	15	US-10-292-088-60	Sequence 60, Appli
45	542	92.8	112	15	US-10-292-088-94	Sequence 94, Appli

## ALIGNMENTS

## RESULT 1

US-10-330-613-2  
; Sequence 2, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-2

Query Match	100.0%;	Score 584;	DB 14;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 7.3e-46;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	DIWVTSPLSLPTGPEPASISCRSSQSLRSNGYLDWYLOKPGQSPHLLIYIGSNRA	60	
Db	1	DIWVTSPLSLPTGPEPASISCRSSQSLRSNGYLDWYLOKPGQSPHLLIYIGSNRA	60	
Qy	61	SGVPDRFSGSGSTDTFTLKISRVAEDVGYVCWQAQSPITFGGTRLEIK	112	
Db	61	SGVPDRFSGSGSTDTFTLKISRVAEDVGYVCWQAQSPITFGGTRLEIK	112	

## RESULT 2

```
US-10-330-530-2
; Sequence 2, Application US/10330530
; Publication No. US2003015251A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-2

Query Match      100.0%; Score 584; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.3e-46;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLSLPVTGPGEPAISCRSSQSLRLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLSLPVTGPGEPAISCRSSQSLRLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

RESULT 3
US-10-660-357-2
; Sequence 2, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-2

Query Match      100.0%; Score 584; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.3e-46;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIVMTQSLSLPVTGPGEPAISCRSSQSLRLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLSLPVTGPGEPAISCRSSQSLRLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

RESULT 4
US-11-021-715-93
; Sequence 93, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; FILE REFERENCE: AUTOANTIBODIES AND INHIBITORS THEREOF
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-93

Query Match      95.2%; Score 556; DB 20; Length 112;
Best Local Similarity 94.6%; Pred. No. 2.7e-43;
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIVMTQSLSLPVTGPGEPAISCRSSQSLRLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLSLPVTGPGEPAISCRSSQSLRLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 111
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 111

RESULT 5
US-10-292-088-52
; Sequence 52, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-52

Query Match      94.9%; Score 554; DB 15; Length 112;
Best Local Similarity 94.6%; Pred. No. 4.1e-43;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIVMTQSLSLPVTGPGEPAISCRSSQSLRLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLSLPVTGPGEPAISCRSSQSLRLSNGYNYLDWYLOKPGQSPHLLIYLGSNRA 60

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQSPITFGQGTGLEIK 112

RESULT 6
US-10-292-088-56
; Sequence 56, Application US/10292088
; Publication No. US20030211100A1
```

```
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-56

Query Match          94.9%; Score 554; DB 15; Length 239;
Best Local Similarity 94.6%; Pred. No. 9.1e-43;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Db 21 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNLDWYLOKPGQSPHLLIYLGSNRA 80
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTRLRIK 112
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOTPTFGQGTKEIK 132

RESULT 7
US-10-292-088-104
; Sequence 104, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-104

Query Match          94.7%; Score 553; DB 15; Length 112;
Best Local Similarity 94.6%; Pred. No. 5e-43;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOTPTFGQGTKEIK 112

RESULT 8
US-11-021-715-75
; Sequence 75, Application US/11021715
```

```
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18,
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-75

Query Match          94.7%; Score 553; DB 20; Length 112;
Best Local Similarity 94.6%; Pred. No. 5e-43;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOTPTFGQGTKEIK 112

RESULT 9
US-11-021-715-90
; Sequence 90, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-90

Query Match          94.7%; Score 553; DB 20; Length 112;
Best Local Similarity 94.6%; Pred. No. 5e-43;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNLDWYLOKPGQSPHLLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLRLRSNGYNLDWYLOKPGQSPHLLIYLGSHRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOSPITFGQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCMQAQOTPTFGQGTKEIK 112
```

## RESULT 10

US-11-021-715-74  
; Sequence 74, Application US/11021715  
; Publication No. US20050208596A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET  
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: 053893-5050  
; CURRENT APPLICATION NUMBER: US/11/021,715  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: PCT/US03/21304  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,352  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/411,694  
; PRIOR FILING DATE: 2002-09-18  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.12  
; SEQ ID NO 74  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-715-74

Query Match 94.5%; Score 552; DB 20; Length 112;  
Best Local Similarity 94.6%; Pred. No. 6.2e-43;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGOSPHLLIYLGNSRA 60  
Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGOSPHLLIYLGNSRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112

## RESULT 11

US-11-021-715-86  
; Sequence 86, Application US/11021715  
; Publication No. US20050208596A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET  
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: 053893-5050  
; CURRENT APPLICATION NUMBER: US/11/021,715  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: PCT/US03/21304  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,352  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/411,694  
; PRIOR FILING DATE: 2002-09-18  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 86  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-715-86

Query Match 94.5%; Score 552; DB 20; Length 112;  
Best Local Similarity 95.5%; Pred. No. 6.2e-43;  
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGOSPHLLIYLGNSRA 60  
Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGOSPHLLIYLGNSRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112

## Db 61

SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112

## RESULT 12

US-10-858-855-8  
; Sequence 8, Application US/10858855  
; Publication No. US20050118651A1  
; GENERAL INFORMATION:  
; APPLICANT: BASI, Guriq  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA  
; TITLE OF INVENTION: AMYLOID PEPTIDE  
; FILE REFERENCE: ELN-028  
; CURRENT APPLICATION NUMBER: US/10/858,855  
; CURRENT FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: 60/474654  
; PRIOR FILING DATE: 2003-05-30  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(22)  
US-10-858-855-8

Query Match 94.5%; Score 552; DB 17; Length 134;  
Best Local Similarity 93.8%; Pred. No. 7.5e-43;  
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGOSPHLLIYLGNSRA 60  
Db 23 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGOSPHLLIYLGNSRA 82  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 112  
Db 83 SGVPDRFSGSGGTDFTLKISRVEAEDGVGYVYCMQAQSPITFGQGTGLEIK 134

## RESULT 13

US-11-021-715-87  
; Sequence 87, Application US/11021715  
; Publication No. US20050208596A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET  
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: 053893-5050  
; CURRENT APPLICATION NUMBER: US/11/021,715  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: PCT/US03/21304  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,352  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/411,694  
; PRIOR FILING DATE: 2002-09-18  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 87  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-715-87

Query Match 94.3%; Score 551; DB 20; Length 112;  
Best Local Similarity 94.6%; Pred. No. 7.7e-43;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGOSPHLLIYLGNSRA 60  
Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLLSNGYNYLDWYLOKPGOSPHLLIYLGNSRA 60



Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQGTREIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQGTREIK 112

RESULT 14

US-11-021-715-89  
; Sequence 89, Application US/11021715  
; Publication No. US20050208596A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET  
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: 053893-5050  
; CURRENT APPLICATION NUMBER: US/11/021.715  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: PCT/US03/21304  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,352  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/411,694  
; PRIOR FILING DATE: 2002-09-18  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 89  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-715-89

Query Match 94.1%; Score 549.5; DB 20; Length 113;  
Best Local Similarity 94.7%; Pred. No. 1.1e-42;  
Matches 107; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 DIVMTQSLPLPVTGPGPASTSCRSSQSLHNSGYNVLDWYLOKPGOSPILLIYLGSNRA 60  
Db 1 DIVMTQSLPLPVTGPGPASTSCRSSQSLHNSGYNVLDWYLOKPGOSPILLIYLGSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQGTREIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQGTREIK 113

RESULT 15

US-10-292-088-103  
; Sequence 103, Application US/10292088  
; Publication No. US2003021100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292.088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 103  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-103

Query Match 93.8%; Score 548; DB 15; Length 112;  
Best Local Similarity 93.8%; Pred. No. 1.4e-42;  
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSLPLPVTGPGPASTSCRSSQSLHNSGYNVLDWYLOKPGOSPILLIYLGSNRA 60

Db 1 DIVMTQSLPLPVTGPGPASTSCRSSQSLHNSGYNVLDWYLOKPGOSPILLIYLGSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQGTREIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQAQSPITFGQGTREIK 112

Search completed: November 16, 2005, 23:05:39  
Job time : 69.7647 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-6

Perfect score: 555

Sequence: 1 EIVMTQSPATLSVSPGERAT.....COQYNNWPRTFQGTQKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003Bs:\*

8: Geneseqp2004s:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	107	7	Adc99777 Anti-huma
2	555	100.0	107	7	Add05381 Anti-MUC1
3	555	100.0	107	7	Adf09819 Human ant
4	546	98.4	107	7	Adc99805 Anti-huma
5	546	98.4	107	7	Adg05409 Anti-MUC1
6	546	98.4	107	7	Add05442 Anti-MUC1
7	546	98.4	107	7	Adf09847 Human ant
8	543	97.8	107	6	Abr54896 Light cha
9	539	97.1	107	6	Abr54900 Light cha
10	536	96.6	107	6	Abr54897 Light cha
11	536	96.6	107	6	Abr54883 Light cha
12	536	96.6	107	8	Adp22404 Human ant
13	536	96.6	107	8	Adp22407 Human ant
14	536	96.6	107	8	Adr43402 Human ant
15	536	96.6	107	8	Adr31547 Light cha
16	534	96.2	107	6	Abr54891 Light cha
17	533	96.1	108	6	Abr54906 Light cha
18	533	96.0	107	6	Abr54893 Light cha
19	533	96.0	107	8	Adp22408 Human ant
20	532	95.9	250	5	Abp45941 Human Bly
21	532	95.9	250	7	Adg96768 Single ch
22	529.5	95.4	117	3	Aay99557 Human Lh1
23	529.5	95.4	117	6	Abr42856 Tumour-sp
24	529.5	95.4	117	6	Abr42858 Tumour-sp
25	529.5	95.4	117	6	Abr42860 Tumour-sp

26	529.5	95.4	117	6	ABR42857	Abr42857 Tumour-sp
27	529.5	95.4	117	7	ABW02446	Abw02446 Human mon
28	529.5	95.4	117	7	ABW02466	Abw02466 Human mon
29	529.5	95.4	117	7	ABW02465	Abw02465 Human mon
30	529	95.3	246	5	ABP45257	Abp45257 Human Bly
31	529	95.3	246	7	ADG96084	Adg96084 Single ch
32	528	95.1	107	6	ABR54889	Abr54889 Light cha
33	526	94.8	107	7	ADJ80364	Adj80364 Human ant
34	525	94.6	107	8	ADP22240	Adp22240 Human ant
35	525	94.6	107	8	ADP22278	Adp22278 Human ant
36	525	94.6	127	7	ADG61110	Adg61110 Human ant
37	524.5	94.5	106	8	ADP22371	Adp22371 Human ant
38	524	94.4	154	8	ADL25472	Adl25472 Human mab
39	522.5	94.1	117	6	ABR42850	Abr42850 Tumour-sp
40	522.5	94.1	117	6	ABR42851	Abr42851 Tumour-sp
41	522.5	94.1	117	6	ABR42849	Abr42849 Tumour-sp
42	522.5	94.1	117	6	ABR42853	Abr42853 Tumour-sp
43	522.5	94.1	117	7	ABW02460	Abw02460 Human mon
44	522.5	94.1	117	7	ABW02462	Abw02462 Human mon
45	522.5	94.1	117	7	ABW02459	Abw02459 Human mon

## ALIGNMENTS

## RESULT 1

ADC99777

ID ADC99777 standard; protein; 107 AA.

XX ADC99777;

XX ADC99777;

DT 01-JAN-2004 (first entry)

XX

DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 6.

XX

KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

XX Homo sapiens.

XX

FN WO2003057838-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041581.

XX

PR 28-DEC-2001; 2001US-0346299P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J;

XX

DR WPI; 2003-587113/55.

DR

N-P8DB; ADC99779.

XX

PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.

PT

tumors, cancers, and other malignancies.

PS

Claim 3; SEQ ID NO 6; 78pp; English.

XX

CC The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody

```
CC light chain protein of the invention.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 4e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCOYNNWPRTFGGTKVEIK 107
DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCOYNNWPRTFGGTKVEIK 107

RESULT 2
ID ADD05381 standard; protein; 107 AA.
XX
AC ADD05381;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 6.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
DR N-PSDB; ADD05383.
XX
PS Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 3; SEQ ID NO 6; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 4e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCOYNNWPRTFGGTKVEIK 107
DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCOYNNWPRTFGGTKVEIK 107

RESULT 3
ID ADF09819 standard; protein; 107 AA.
XX
AC ADF09819;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #2.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-598367/56.
DR N-PSDB; ADF09821.
XX
PS Inhibiting cell proliferation associated with expression of MUC18 tumour
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 3; SEQ ID NO 6; 83pp; English.
XX
CC The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
PS Sequence 107 AA;

Query Match      100.0%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 4e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCOYNNWPRTFGGTKVEIK 107
DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCOYNNWPRTFGGTKVEIK 107
```

```

RESULT 4
ADC99805
ID ADC99805 standard; protein; 107 AA.
AC ADC99805;
XX
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 34.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR N-PSDB; ADC99807.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 3; SEQ ID NO 34; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC light chain protein of the invention.
XX
SQ Sequence 107 AA;
Query Match 98.4%; Score 546; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.9e-33;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVNNLAWYQKPGQAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVNNLAWYQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
DB 61 RFGSGSGTFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
RESULT 5
ADD05409
ID ADD05409 standard; protein; 107 AA.
XX
AC ADD05409;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region L2 protein, SEQ ID 67.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
XX

```

```
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX Unidentified.
OS
XX WO2003057006-A2.
PN
XX 17-JUL-2003.
PD
XX 26-DEC-2002; 2002WO-US041582.
PF
XX 28-DEC-2001; 2001US-0346460P.
PR
XX (ABGE-) ABGENIX INC.
XX
XX Gudae J, Bar-Eli M;
PI
XX WPI; 2003-577496/54.
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
XX Disclosure; SEQ ID NO 67; 87pp; English.
PS
XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
XX Sequence 107 AA;
SQ
Query Match 98.4%; Score 546; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.9e-33;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNLAWYQQKPGAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNLAWYQQKPGAPRLIIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWPRFTFGQTKVEIK 107
DB 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWPRFTFGQTKVEIK 107
RESULT 7
ADF09847
ID ADF09847 standard; protein; 107 AA.
XX
AC ADF09847;
XX
XX 12-FEB-2004 (first entry)
DT
XX Human anti-MUC18 monoclonal antibody light chain #9.
DE
XX cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
XX Homo sapiens.
OS
XX WO2003057837-A2.
XX
XX
```

---

```
XX
PD 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041580.
PF
XX 28-DEC-2001; 2001US-0346414P.
PR
XX (ABGE-) ABGENIX INC.
XX
XX Gudae J;
PI
XX WPI; 2003-598367/56.
DR N-PSDB; ADF09849.
XX
XX Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
XX Claim 3; SEQ ID NO 34; 83pp; English.
PS
XX The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
XX Sequence 107 AA;
SQ
Query Match 98.4%; Score 546; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.9e-33;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNLAWYQQKPGAPRLIIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNLAWYQQKPGAPRLIIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWPRFTFGQTKVEIK 107
DB 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWPRFTFGQTKVEIK 107
RESULT 8
ABR54896
ID ABR54896 standard; protein; 107 AA.
XX
AC ABR54896;
XX
XX 30-JUN-2003 (first entry)
DT
XX Light chain clone HBPAXK2d 3A9 SEQ ID NO:122.
DE
XX Engineered template; single primer amplification; antibody library;
KW nucleic acid amplification.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO2003025202-A2.
XX
XX 27-MAR-2003.
PD
XX 19-SEP-2002; 2002WO-US029889.
PF
XX 19-SEP-2001; 2001US-0323455P.
PR
XX (ALEX-) ALEXION PHARM INC.
XX
XX Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
```

```

XX DR WPI; 2003-313359/30.
XX PT Amplifying nucleic acid by contacting engineered nucleic acid strand
XX PT having predetermined sequence at one end and sequence complementary to
XX PT predetermined sequence at other end, with primer having predetermined
XX PT sequence.
XX PS Example 3; Fig 8b-c; 68pp; English.
XX CC The present invention describes a method (M1) for amplifying a nucleic
XX CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other, and contacting (S) with a
XX CC primer having the predetermined sequence in the presence of a polymers
XX CC and nucleotides under conditions suitable for polymerisation of the
XX CC nucleotides. Also described is an engineered nucleic acid strand (I)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other end. M1 is useful for
XX CC amplifying a nucleic acid. M1 can be used for producing an antibody
XX CC library. M1 is useful for preparing amplified products that can be
XX CC ligated into a suitable expression vector, where the vector can be used
XX CC to transform an appropriate host organism to produce the polypeptide or
XX CC protein encoded by the target sequence. M1 is useful to amplify a family
XX CC of related sequences to build a complex library such as, for example an
XX CC antibody library. M1 is useful not only for producing large amounts of
XX CC one target nucleic acid sequence, but also for amplifying simultaneously
XX CC more than one different target nucleic acid sequence located on the same
XX CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
XX CC ABR54998 represent sequence used in the exemplification of the present
XX CC invention
XX SQ Sequence 107 AA;
XX
XX Query Match 97.8%; Score 543; DB 6; Length 107;
XX Best Local Similarity 98.1%; Pred. No. 3.1e-33;
XX Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
DB |||||
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYQCQYNNWPTFGQGTKVEIK 107
DB |||||
DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYQCQYNNWPTFGQGTKVEIK 107

RESULT 9
ABR54900
ID ABR54900 standard; protein; 107 AA.
XX AC ABR54900;
XX DT 30-JUN-2003 (first entry)
XX DE Light chain clone HBPAXK2d 3D12 SEQ ID NO:126.
XX KW Engineered template; single primer amplification; antibody library;
XX KW nucleic acid amplification.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003025202-A2.
XX PD 27-MAR-2003.
XX PF 19-SEP-2002; 2002WO-US029889.
XX PR 19-SEP-2001; 2001US-0323455P.
XX PA (ALEX-) ALEXION PHARM INC.
XX

PI Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
XX WPI; 2003-313359/30.
XX PT Amplifying nucleic acid by contacting engineered nucleic acid strand
XX PT having predetermined sequence at one end and sequence complementary to
XX PT predetermined sequence at other end, with primer having predetermined
XX PT sequence.
XX PS Example 3; Fig 8b-c; 68pp; English.
XX CC The present invention describes a method (M1) for amplifying a nucleic
XX CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other, and contacting (S) with a
XX CC primer having the predetermined sequence in the presence of a polymers
XX CC and nucleotides under conditions suitable for polymerisation of the
XX CC nucleotides. Also described is an engineered nucleic acid strand (I)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other end. M1 is useful for
XX CC amplifying a nucleic acid. M1 can be used for producing an antibody
XX CC library. M1 is useful for preparing amplified products that can be
XX CC ligated into a suitable expression vector, where the vector can be used
XX CC to transform an appropriate host organism to produce the polypeptide or
XX CC protein encoded by the target sequence. M1 is useful to amplify a family
XX CC of related sequences to build a complex library such as, for example an
XX CC antibody library. M1 is useful not only for producing large amounts of
XX CC one target nucleic acid sequence, but also for amplifying simultaneously
XX CC more than one different target nucleic acid sequence located on the same
XX CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
XX CC ABR54998 represent sequence used in the exemplification of the present
XX CC invention
XX SQ Sequence 107 AA;
XX
XX Query Match 97.1%; Score 539; DB 6; Length 107;
XX Best Local Similarity 97.2%; Pred. No. 6.2e-33;
XX Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
DB |||||
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYQCQYNNWPTFGQGTKVEIK 107
DB |||||
DB 61 RPSGSGSGTEFTLTISLSQSEDFAVYQCQYNNWPTFGQGTKVEIK 107

RESULT 10
ABR54897
ID ABR54897 standard; protein; 107 AA.
XX AC ABR54897;
XX DT 30-JUN-2003 (first entry)
XX DE Light chain clone HBPAXK2d 3A12 SEQ ID NO:123.
XX KW Engineered template; single primer amplification; antibody library;
XX KW nucleic acid amplification.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003025202-A2.
XX PD 27-MAR-2003.
XX PF 19-SEP-2002; 2002WO-US029889.
XX PR 19-SEP-2001; 2001US-0323455P.
XX PA (ALEX-) ALEXION PHARM INC.
XX

```

XX Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;  
 XX WPI; 2003-313359/30.  
 XX  
 XX Amplifying nucleic acid by contacting engineered nucleic acid strand  
 PT having predetermined sequence at one end and sequence complementary to  
 PT predetermined sequence at other end, with primer having predetermined  
 PT sequence.  
 XX  
 XX Example 3; Fig 8b-c; 68pp; English.  
 XX  
 XX The present invention describes a method (M1) for amplifying a nucleic  
 CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)  
 CC having a predetermined sequence at one end and a sequence complementary  
 CC to the predetermined sequence at the other, and contacting (S) with a  
 CC primer having the predetermined sequence in the presence of a polymers  
 CC and nucleotides under conditions suitable for polymerisation of the  
 CC nucleotides. Also described is an engineered nucleic acid strand (I)  
 CC having a predetermined sequence at one end and a sequence complementary  
 CC to the predetermined sequence at the other end. M1 is useful for  
 CC amplifying a nucleic acid. M1 can be used for producing an antibody  
 CC library. M1 is useful for preparing amplified products that can be  
 CC ligated into a suitable expression vector, where the vector can be used  
 CC to transform an appropriate host organism to produce the polypeptide or  
 CC protein encoded by the target sequence. M1 is useful to amplify a family  
 CC of related sequences to build a complex library such as, for example an  
 CC antibody library. M1 is useful not only for producing large amounts of  
 CC one target nucleic acid sequence, but also for amplifying simultaneously  
 CC more than one different target nucleic acid sequence located on the same  
 CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to  
 CC ABR54998 represent sequence used in the exemplification of the present  
 CC invention  
 XX  
 XX Sequence 107 AA;  
 SQ  
 Query Match 96.6%; Score 536; DB 6; Length 107;  
 Best Local Similarity 96.3%; Pred. No. 1e-32;  
 Matches 103; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLLIYGASTRATGIPA 60  
 Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLLIYGASTRATGIPA 60  
 OY 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWNPRTFGGTKEIK 107  
 Db 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWNPRTFGGTKEIK 107  
 RESULT 11  
 ABR54883  
 ID ABR54883 standard; protein; 107 AA.  
 XX  
 AC ABR54883;  
 XX  
 XX 30-JUN-2003 (first entry)  
 DT  
 DE Light chain clone HBPAXK1b 3A2 SEQ ID NO:109.  
 XX  
 XX Engineered template; single primer amplification; antibody library;  
 KW nucleic acid amplification.  
 KW  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO2003025202-A2.  
 PN  
 XX 27-MAR-2003.  
 PD  
 XX 19-SEP-2002; 2002WO-US029889.  
 PF  
 XX 19-SEP-2001; 2001US-0323455P.  
 PR  
 XX

PA (ALEX-) ALEXION PHARM INC.  
 XX Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;  
 XX WPI; 2003-313359/30.  
 DR  
 XX Amplifying nucleic acid by contacting engineered nucleic acid strand  
 PT having predetermined sequence at one end and sequence complementary to  
 PT predetermined sequence at other end, with primer having predetermined  
 PT sequence.  
 XX  
 XX Example 3; Fig 8b-c; 68pp; English.  
 PS  
 XX The present invention describes a method (M1) for amplifying a nucleic  
 CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)  
 CC having a predetermined sequence at one end and a sequence complementary  
 CC to the predetermined sequence at the other, and contacting (S) with a  
 CC primer having the predetermined sequence in the presence of a polymers  
 CC and nucleotides under conditions suitable for polymerisation of the  
 CC nucleotides. Also described is an engineered nucleic acid strand (I)  
 CC having a predetermined sequence at one end and a sequence complementary  
 CC to the predetermined sequence at the other end. M1 is useful for  
 CC amplifying a nucleic acid. M1 can be used for producing an antibody  
 CC library. M1 is useful for preparing amplified products that can be  
 CC ligated into a suitable expression vector, where the vector can be used  
 CC to transform an appropriate host organism to produce the polypeptide or  
 CC protein encoded by the target sequence. M1 is useful to amplify a family  
 CC of related sequences to build a complex library such as, for example an  
 CC antibody library. M1 is useful not only for producing large amounts of  
 CC one target nucleic acid sequence, but also for amplifying simultaneously  
 CC more than one different target nucleic acid sequence located on the same  
 CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to  
 CC ABR54998 represent sequence used in the exemplification of the present  
 CC invention  
 XX  
 XX Sequence 107 AA;  
 SQ  
 Query Match 96.6%; Score 536; DB 6; Length 107;  
 Best Local Similarity 96.3%; Pred. No. 1e-32;  
 Matches 103; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLLIYGASTRATGIPA 60  
 Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLLIYGASTRATGIPA 60  
 OY 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWNPRTFGGTKEIK 107  
 Db 61 RFGSGSGTFTLTISLSQSEDFAVYYCQYNNWNPRTFGGTKEIK 107  
 RESULT 12  
 ADP22404  
 ID ADP22404 standard; protein; 107 AA.  
 XX  
 AC ADP22404;  
 XX  
 XX 09-SEP-2004 (first entry)  
 DT  
 DE Human anti-TNFA antibody light chain variable region SEQ ID NO:310.  
 XX  
 XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.  
 XX



OS Homo sapiens.  
 XX WO2004050683-A2.  
 XX 17-JUN-2004.  
 XX 02-DEC-2003; 2003WO-US038281.  
 XX 02-DEC-2002; 2002US-0430729P.  
 XX (ABGE-) ABGENIX INC.  
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX WPI; 2004-480601/45.  
 XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX Example 10; SEQ ID NO 310; 213pp; English.  
 XX The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFa in a patient sample, comprising contacting with  
 CC the sample; (2) a composition comprising the antibody and TNFa in  
 CC the sample; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFa induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoaric, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic, and  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFa  
 CC antibody light chain variable region, which is used in the  
 XX exemplification of the present invention.  
 SQ Sequence 107 AA;  
 Query Match 96.6%; Score 536; DB 8; Length 107;  
 Best Local Similarity 96.3%; Pred. No. 1e-32;  
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQQKPGQAPRLIYYGASTRATGIPA 60  
 DB 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQQKPGQAPRLIYYGASTRATGIPA 60  
 QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQQYNNWPRFTGGTKVEIK 107  
 DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQQYNNWPRFTGGTKVEIK 107

RESULT 13  
 ADP22407

ID ADP22407 standard; protein; 107 AA.  
 XX AC ADP22407;  
 XX DT 09-SEP-2004 (first entry)  
 XX DE Human anti-TNPa antibody light chain variable region SEQ ID NO:313.  
 XX KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
 KW anti-TNPa antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoaric; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.  
 XX OS Homo sapiens.  
 XX PN WO2004050683-A2.  
 XX PD 17-JUN-2004.  
 XX PF 02-DEC-2003; 2003WO-US038281.  
 XX PR 02-DEC-2002; 2002US-0430729P.  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX WPI; 2004-480601/45.  
 XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX Example 10; SEQ ID NO 313; 213pp; English.  
 XX The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFa in a patient sample, comprising contacting with  
 CC the sample; (2) a composition comprising the antibody and TNFa in  
 CC the sample; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFa induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoaric, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic, and  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis, and disease, graft-host reactions, septic shock, cachexia, anorexia, and

CC multiple sclerosis. The present sequence represents a human anti-TNFa  
CC antibody light chain variable region, which is used in the  
CC exemplification of the present invention.

XX SQ Sequence 107 AA;

Query Match 96.6%; Score 536; DB 8; Length 107;  
Best Local Similarity 97.2%; Pred. No. 1e-32;  
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60  
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 14

ADR43402 standard; protein; 107 AA.

XX ID ADR43402;

XX AC ADR43402;

XX DT 04-NOV-2004 (first entry)

XX DE Human anti-IgE antibody light chain L16 and JK4.

XX KW antibody; variable light chain; variable heavy chain; Antiallergic;

XX KM Dermatological; Immunosuppressive; IGE; asthma; allergic rhinitis;

XX KW eczema; urticaria; atopic dermatitis; food allergy; CDR.

XX OS Homo sapiens.

XX PN WO2004070011-A2.

XX PD 19-AUG-2004.

XX PF 02-FEB-2004; 2004WO-US002894.

XX PR 01-FEB-2003; 2003US-0444229P.

XX PA (TANO-) TANOX INC.

XX PI Singh S, Foster C, Wu H;

XX PS WPI; 2004-604433/58.

XX PT New high affinity human monoclonal antibodies, particularly those  
PT directed against isotypic determinants of immunoglobulin E, useful for  
PT asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a  
PT food allergy.

XX PS Disclosure; SEQ ID NO 2; 101pp; English.

XX CC The present invention relates to an antibody comprising a variable light  
CC chain region or a variable heavy chain region. The antibody and methods  
CC are useful for treating a disorder associated with an abnormally high Ige  
CC level, e.g. asthma, allergic rhinitis, eczema, urticaria, atopic  
CC dermatitis, or a food allergy. The present sequence represents human anti  
CC -Ige antibody light chain combined L16 and JK4.

XX SQ Sequence 107 AA;

Query Match 96.6%; Score 536; DB 8; Length 107;  
Best Local Similarity 97.2%; Pred. No. 1e-32;  
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60  
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 15

ADR31547 standard; protein; 107 AA.

XX ID ADR31547;

XX AC ADR31547;

XX DT 04-NOV-2004 (first entry)

XX DE L16/JK4 human light chain consensus sequence template.

XX KW Antibody; diagnostic; prophylaxis; therapy; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 24..34 /note= "Kabat CDR"

FT Region 50..56 /note= "Kabat CDR"

FT Region 89..97 /note= "Kabat CDR"

XX PN WO2004070010-A2.

XX PD 19-AUG-2004.

XX PF 02-FEB-2004; 2004WO-US002892.

XX PR 01-FEB-2003; 2003US-0444229P.

XX PA (TANO-) TANOX INC.

XX PI Singh S, Foster C, Wu H;

XX PS WPI; 2004-604432/58.

XX PT Generating a humanized, high affinity antibody from an antibody of  
PT interest comprises selecting a suitable human template as the framework  
PT for the H and L chain variable domains of the high affinity antibody to  
PT be made.

XX PS Example 1; SEQ ID NO 2; 100pp; English.

XX CC The invention relates to a method for generating a humanised high  
CC affinity antibody from an antibody of interest. The method involves  
CC selecting a suitable human template as the framework for the H (heavy)  
CC and L (light) chain variable (V) domains of the high affinity antibody to  
CC be made. The method is useful for generating high affinity antibodies  
CC useful in diagnostics, prophylaxis and treatment of diseases. The present  
CC sequence is L16/JK4 human light chain consensus sequence template. This  
CC sequence is used in the exemplification of the invention.

XX SQ Sequence 107 AA;

Query Match 96.6%; Score 536; DB 8; Length 107;  
Best Local Similarity 97.2%; Pred. No. 1e-32;  
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60  
DB 1 EIVMTQSPATLSVSPGERATLSCRSQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

Search completed: November 16, 2005, 21:51:36

Job time : 62.3676 secs

CHINA 2011-2012

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-6  
Perfect score: 555  
Sequence: 1 EIVMTQSPATLSVSPGERAT.....COQYNWPRTFQGTKEIK 107  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	544	98.0	107	S34005	Ig kappa chain V r
2	536	96.6	117	S40362	Ig kappa chain - h
3	531	95.7	128	S40343	Ig kappa chain V-J
4	508.5	91.6	109	A330PM	Ig kappa chain V-I
5	499.5	90.0	131	S40328	Ig kappa chain - h
6	495	89.2	128	A56701	Ig kappa chain V r
7	493.5	88.9	116	B26555	Ig kappa chain V-I
8	491	88.5	111	S23628	Ig kappa chain V r
9	490.5	88.4	215	JE0244	Ig kappa chain NIG
10	484	87.2	115	K3H0CL	Ig kappa chain pre
11	483	87.0	115	A30553	Ig kappa chain pre
12	482	86.8	144	PL0106	Ig kappa chain pre
13	481	86.7	215	JE0243	Ig kappa chain NIG
14	473.5	85.3	109	D30601	Ig kappa chain V-I
15	473	85.2	95	PH0868	Ig kappa chain V r
16	473	85.1	98	I30608	Ig kappa chain V-I
17	472.5	85.1	114	S54905	Ig kappa chain V r
18	472.5	85.1	129	K3HUHA	Ig kappa chain pre
19	471	84.9	110	S40326	Ig kappa chain V-J
20	471	84.9	123	S40378	Ig kappa chain - h
21	471	84.9	128	S40379	Ig kappa chain V-J
22	470.5	84.8	109	F30607	Ig kappa chain V-I
23	468	84.3	91	S37527	Ig kappa chain V r
24	468	84.3	108	G44151	Ig kappa chain V r
25	467.5	84.2	109	K3HUSI	Ig kappa chain V-I
26	467.5	84.2	109	S30601	Ig kappa chain V-I
27	466.5	84.1	109	B30601	Ig kappa chain V-I
28	466.5	84.1	128	S20636	Ig kappa chain V r
29	465.5	83.9	129	A32274	Ig kappa chain pre

30	464.5	83.7	110	2	S20635	Ig kappa chain V r
31	463.5	83.5	109	2	H30601	Ig kappa chain V-I
32	463.5	83.5	109	2	C30601	Ig kappa chain V-I
33	462.5	83.3	108	2	C30608	Ig kappa chain V-I
34	461.5	83.2	109	1	K3HUTI	Ig kappa chain V-I
35	461.5	83.2	109	2	PH0963	Ig kappa chain V r
36	461.5	83.2	129	2	S49532	anti-Sm antibody V
37	460.5	83.0	109	1	K3HUWL	Ig kappa chain V-I
38	459.5	82.8	109	2	A30608	Ig kappa chain V-I
39	459.5	82.8	129	1	K3HUIH	Ig kappa chain pre
40	459	82.7	129	2	S29627	Ig kappa chain V r
41	458	82.5	107	2	S57444	Ig kappa chain V-J
42	456.5	82.3	215	2	JE0242	Ig kappa chain NIG
43	455	82.0	106	2	PC4282	Ig kappa chain (an
44	455	82.0	128	2	S40345	Ig kappa chain V-J
45	454.5	81.9	109	2	F30601	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S34005  
Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S34005; S30524  
R:Mariette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993.  
A>Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A:Reference number: S34001; MUID:93209281; PMID:7681398  
A:Accession: S34005  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-107 <MAR>  
A:Cross-references: EMBL:X18330  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 544; DB 2; Length 107;  
Best Local Similarity 98.1%; Pred. No. 3.4e-39;  
Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA	60
DB	1	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA	60
QY	61	RFSGSGSGTEFTLTISSLQSEDFAVYCCQYNWPRTFQGTKEIK	107
DB	61	RFSGSGSGTEFTLTISSLQSEDFAVYCCQYNWPRTFQGTKEIK	107

RESULT 2

S40362  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40362  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40362  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-117 <KLE>  
A:Cross-references: EMBL:X72472; NID:g441412; PID:g441413  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 96.6%; Score 536; DB 2; Length 117;

Best Local Similarity 97.2%; Pred. No. 1.7e-38; Mismatches 1; Indels 2; Gaps 0;  
Matches 104; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
DB 11 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 70  
QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107  
DB 71 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 117

## RESULT 3

S40343  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40343  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40343  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-128 <KLE>  
A:Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 531; DB 2; Length 128;  
Best Local Similarity 95.3%; Pred. No. 5e-38; Mismatches 3; Indels 2; Gaps 0;  
Matches 102; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
DB 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 80  
QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107  
DB 81 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 127

## RESULT 4

K3HUPM  
Ig kappa chain V-III region (Pom) - human (tentative sequence)  
C:Species: Homo sapiens (man)  
C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C:Accession: A01897  
R:Klapper, D.G.; Capra, J.D.  
Ann. Immunol. (Inst. Pasteur) 127C, 261-271, 1976  
A:Title: The amino acid sequence of the variable regions of the light chains from two id  
A:Reference number: A01897  
A:Accession: A01897  
A:Molecule type: protein  
A:Residues: 1-109 <KLA>  
A:Cross-references: UNIPROT:P01624  
C:Comment: This chain was isolated from an IgM with anti-gamma globulin activity.  
C:Genetics:  
A:Gene: GDB:IGKV3  
A:Cross-references: GDB:136266  
A:Map position: 2p12-2p11  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k) h  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F;15-91/Domain: immunoglobulin homology <IMM>  
F;23-89/Disulfide bonds: #status predicted

Query Match 91.6%; Score 508.5; DB 1; Length 109;  
Best Local Similarity 91.7%; Pred. No. 3.4e-36; Mismatches 4; Indels 1; Gaps 1;  
Matches 99; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIP 59  
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIP 60  
QY 60 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107  
DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 108

## RESULT 5

S40328  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40328  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40328  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-131 <KLE>  
A:Cross-references: EMBL:X72438; NID:g441344; PIDN:CAA51106.1; PID:g441345  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;35-109/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 499.5; DB 2; Length 131;  
Best Local Similarity 89.8%; Pred. No. 2.3e-35; Mismatches 4; Indels 1; Gaps 1;  
Matches 97; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
DB 20 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 79  
QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107  
DB 80 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 127

## RESULT 6

A56701  
Ig kappa chain V region precursor (HuA) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jan-2000  
C:Accession: A56701  
R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.  
J. Biol. Chem. 270, 12457-12465, 1995  
A:Title: Human and mouse monoclonal antibodies to blood group A substance, which are near  
A:Reference number: A56701; MUID:95279371; PMID:7759488  
A:Accession: A56701  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-128 <NIC>  
A:Cross-references: GB:I41174; NID:g762823; PIDN:AAA64877.1; PID:g762824  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 495; DB 2; Length 128;  
Best Local Similarity 88.8%; Pred. No. 5.3e-35; Mismatches 7; Indels 5; Gaps 0;  
Matches 95; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
DB 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 80  
QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 107  
DB 81 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRFTFGQGTKEIK 127

```
RESULT 7
B26555
Ig kappa chain V-III region (Ger) - human
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26555
R:Widdaugh, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A:Title: Atypical glycosylation of an Igg monoclonal cryoimmunoglobulin.
A:Reference number: A92630; MUID:87137666; PMID:3102493
A:Accession: B26555
A:Molecule type: protein
A:Residues: 1-116 <MID>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMW>

Query Match      88.9%; Score 493.5; DB 2; Length 116;
Best Local Similarity 88.9%; Pred. No. 6.5e-35;
Matches 96; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

QY 1 EVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 DIVMTQVPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYAASRATGIPA 60

QY 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWP-TEGQGTKEIK 107
Db 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWPITFGQGTKEIK 108

RESULT 8
S23628
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S23628
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A:Reference number: S23623; MUID:92156804; PMID:1740865
A:Accession: S23628
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <OLE>
A:Cross-references: EMBL:X59705; NID:G34022; PIDN:CAA42226.1; PID:gl335190
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMW>

Query Match      88.5%; Score 491; DB 2; Length 111;
Best Local Similarity 88.8%; Pred. No. 1e-34;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 EVLTQSPATLSVSPGERATLSCRASQSVSVLAWYQOKPGQAPRLIIYDASNRATGIPA 60

QY 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWPTEGQGTKEIK 107
Db 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWPITFGQGTKEIK 107

RESULT 9
JE0244
Ig kappa chain IIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, H.;
submitted to JFID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A:Reference number: JE0243
```

```
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMW>

Query Match      88.4%; Score 490.5; DB 2; Length 215;
Best Local Similarity 88.9%; Pred. No. 2.1e-34;
Matches 96; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 EVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 EVLTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYFRASTRATGIPA 60

QY 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWP-PRTEGQGTKEIK 107
Db 61 RFGSGSGTFTLTISLQSEDFALYVCOQYNTWPLTFGGGTKEIK 108

RESULT 10
K3HUCL
Ig kappa chain precursor V-III region (CLL) - human
N:Alternate names: rheumatoid factor
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C:Accession: A01898
R:Jirik, F.R.; Sorge, J.; Fong, S.; Heitzmann, J.G.; Curd, J.G.; Chen, P.P.; Goldfien, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
A:Title: Cloning and sequence determination of a human rheumatoid factor light-chain gene
A:Reference number: A01898; MUID:86177570; PMID:3083417
A:Accession: A01898
A:Molecule type: DNA
A:Residues: 1-115 <JIR>
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:I36266
A:Map position: 2p12-2p11
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as Iga and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: rheumatoid factor, Ig kappa chain V-III region (CLL) #status predicted
F:21-43/Region: framework 1
F:36-110/Domain: immunoglobulin homology <IMW>
F:44-54/Region: complementarity-determining 1
F:55-69/Region: framework 2
F:70-76/Region: complementarity-determining 2
F:77-108/Region: framework 3
F:109-115/Region: complementarity-determining 3
F:43-108/Disulfide bonds: #status predicted

Query Match      87.2%; Score 484; DB 1; Length 115;
Best Local Similarity 97.9%; Pred. No. 4.1e-34;
Matches 93; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 21 EVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 80

QY 61 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWP 95
Db 81 RFGSGSGTFTLTISLQSEDFAVYVCOQYNNWP 115

RESULT 11
A30553
Ig kappa chain precursor V-III region (Hah) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: A30553
```

R;Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson, D.  
J. Immunol. 142, 688-694, 1989  
A;Title: Characterization of four homologous L chain variable region genes that are rela  
A;Reference number: A30553; MUID:89093959; PMID:2492051  
A;Accession: A30553  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-115 <LU>  
A;Note: the sequence was determined from the differentiated gene  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 483; DB 2; Length 115;  
Best Local Similarity 97.9%; Pred. No. 4.9e-34; Indels 0; Gaps 0;  
Matches 93; Conservative 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
DB 21 EIVMQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 80  
61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWP 95  
81 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWP 115

RESULT 12  
PL0106  
IG kappa chain precursor V-J-C region (LS1) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000  
C;Accession: PL0106  
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.  
J. Exp. Med. 169, 1631-1643, 1989  
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma sec  
A;Reference number: PL0106; MUID:89235583; PMID:2541221  
A;Accession: PL0106  
A;Molecule type: mRNA  
A;Residues: 1-144 <SL>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-115/Domain: V region <VRE>  
F;36-110/Domain: immunoglobulin homology <IMM>  
F;44-54/Region: complementarity-determining 1  
F;70-76/Region: complementarity-determining 2  
F;109-115/Region: complementarity-determining 3  
F;116-127/Domain: J region <JRG>  
F;128-144/Domain: C region (fragment) <CRE>

Query Match 86.8%; Score 482; DB 2; Length 144;  
Best Local Similarity 86.9%; Pred. No. 7.4e-34;  
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
DB 21 EIVLTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYDASNRATGIPA 80  
61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQTKVEIK 107  
81 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPLTFGGTKVEIK 127

RESULT 13  
JE0243  
IG kappa chain NIG93 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C;Accession: JE0243  
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T  
submitted to JIPIB, November 1998  
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy  
A;Reference number: JE0243

A;Accession: JB0243  
A;Molecule type: protein  
A;Residues: 1-215 <ALI>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 481; DB 2; Length 215;  
Best Local Similarity 86.9%; Pred. No. 1.3e-33;  
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYDASTRATGIPA 60  
61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQTKVEIK 107  
61 RFGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPTFGQTKVETK 107

RESULT 14  
D30601  
IG kappa chain V-III region (Cur) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: D30601  
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
J. Immunol. 142, 3158-3163, 1989  
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantib  
A;Reference number: A30601; MUID:89215279; PMID:2496160  
A;Accession: D30601  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-109 <GON>  
A;Cross-references: UNIPROT:Q9UL78  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 473.5; DB 2; Length 109;  
Best Local Similarity 86.1%; Pred. No. 3e-33;  
Matches 93; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIP 59  
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAQYQKPGQAPRLIIYGASSRATGIP 60  
60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQTKVEIK 107  
61 DRFSGSGSGTEFTLTISRLPEDFAVYYCQYQYSGSPRTFGQTKVEIK 108

RESULT 15  
PH0868  
IG kappa chain V region (anti-DNA, II-1) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 21-Jan-2000  
C;Accession: PH0868  
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.  
J. Exp. Med. 174, 1639-1652, 1991  
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype  
A;Reference number: PH0862; MUID:92078875; PMID:1660528  
A;Accession: PH0868  
A;Molecule type: DNA  
A;Residues: 1-95 <MAN>  
A;Note: the authors translated the codon CTC for residue 73 as Phe  
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-23/Region: framework 1  
F;16-90/Domain: immunoglobulin homology <IMM>  
F;24-34/Region: complementarity-determining 1  
F;35-49/Region: framework 2  
F;50-56/Region: complementarity-determining 2



```

F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

Query Match      85.2%; Score 473; DB 2; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.9e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db      1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60

Qy      61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNWP 95
Db      61 RISGSGSGTEFTLTISLSQSEDFAVYCCQYNWP 95

```

Search completed: November 16, 2005, 22:04:06  
Job time : 12.7849 secs

©2007 2007 10 10 10 10

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-6  
Perfect score: 555  
Sequence: 1 E1WQTSPATLSVSPGERAT.....CQYNNWPTFGGKTKEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	524.5	94.5	129	1 KV3H_HUMAN	P04207 homo sapien
2	513	92.4	108	2 Q9UL83	Q9ul83 homo sapien
3	508.5	91.6	109	1 KV3F_HUMAN	P01624 homo sapien
4	505.5	91.1	109	2 Q9UL85	Q9ul85 homo sapien
5	495.5	89.3	235	2 Q6GMW0	Q6gmw0 homo sapien
6	472.5	85.1	129	1 KV3L_HUMAN	P18135 homo sapien
7	467.5	84.2	109	1 KV3B_HUMAN	P01620 homo sapien
8	461.5	83.2	109	1 KV3D_HUMAN	P01622 homo sapien
9	460.5	83.0	109	1 KV3E_HUMAN	P01623 homo sapien
10	459.5	82.8	129	1 KV3M_HUMAN	P18136 homo sapien
11	451.5	81.4	109	2 Q9UL78	Q9ul78 homo sapien
12	442.5	79.7	109	1 KV3G_HUMAN	P04206 homo sapien
13	439.5	79.2	108	1 KV3A_HUMAN	P01619 homo sapien
14	438	78.9	115	1 KV3I_HUMAN	P04433 homo sapien
15	436.5	78.6	235	2 Q6GMV9	Q6gmv9 homo sapien
16	434.5	78.3	235	2 Q6RJF2	Q6rjf2 homo sapien
17	434	78.2	128	1 KV3K_HUMAN	P06311 homo sapien
18	432	77.8	108	1 KV1M_HUMAN	P01605 homo sapien
19	432	77.8	236	2 Q6PIL8	Q6pil8 homo sapien
20	431	77.7	236	2 Q6P5S8	Q6p5s8 homo sapien
21	428.5	77.2	109	2 Q9UL86	Q9ul86 homo sapien
22	422	76.0	108	2 Q9UL79	Q9ul79 homo sapien
23	418	75.3	134	1 KV4C_HUMAN	P06314 homo sapien
24	415.5	74.9	116	1 KV3J_HUMAN	P04434 homo sapien
25	408	73.5	114	1 KV4A_HUMAN	P01625 homo sapien
26	407	73.3	108	2 Q9UL70	Q9ul70 homo sapien
27	407	73.3	236	2 Q6GMW1	Q6gmw1 homo sapien
28	405	73.0	108	1 KV1R_HUMAN	P01610 homo sapien
29	405	73.0	236	2 Q6PIH7	Q6pih7 homo sapien
30	405	73.0	236	2 Q6PITS	Q6pits homo sapien
31	404.5	72.9	100	1 KV3C_HUMAN	P01621 homo sapien

Query Match

Score 524.5; DB 1; Length 129;

94.5%;

32	403	72.6	234	2	Q7Z473	Q7z473 homo sapien
33	402.5	72.5	133	1	KV4B_HUMAN	P06313 homo sapien
34	402	72.4	108	1	KV1G_HUMAN	P01599 homo sapien
35	400	72.1	108	1	KV1F_HUMAN	P01598 homo sapien
36	400	72.1	108	1	KV1V_HUMAN	P04430 homo sapien
37	400	72.1	236	2	Q7Z3Y4	Q7z3y4 homo sapien
38	400	72.1	244	2	Q6SZC8	Q6szc8 homo sapien
39	397	71.5	108	1	KV1L_HUMAN	P01604 homo sapien
40	396	71.4	236	2	Q6GMX8	Q6gmxx8 homo sapien
41	395	71.2	240	2	Q6SZC9	Q6szc9 homo sapien
42	394	71.0	255	2	Q6KB05	Q6kb05 mus musculus
43	393	70.8	108	1	KV1K_HUMAN	P01603 homo sapien
44	393	70.8	108	1	KV1Q_HUMAN	P01609 homo sapien
45	393	70.8	236	2	Q6GMX9	Q6gmxx9 homo sapien

ALIGNMENTS

RESULT 1  
KV3H\_HUMAN STANDARD; PRT; 129 AA.  
AC P04207;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86177570; PubMed=3083417;  
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,  
RA Goldfien R., Carson D.A.;  
RT "Cloning and sequence determination of a human rheumatoid factor  
light-chain gene."  
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
EMBL; M12740; AA58992.1; -.  
HSSP; P01625; 1LVB.  
GO; GO:0005576; C:extracellular; NAS.  
GO; GO:0003823; F:antigen binding; NAS.  
GO; GO:0006955; P:immune response; NAS.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003596; IG\_v.  
Pfam; PF00047; ig; 1.  
SMART; SM00406; Igv; 1.  
PROSITE; PS50835; IG LIKE; 1.  
Immunoglobulin V region; Signal.  
SIGNAL 1 20  
FT CHAIN 21 129 Ig kappa chain V-III region CLL.  
FT DOMAIN 21 43 Framework-1.  
FT DOMAIN 44 54 Complementarity-determining-1.  
FT DOMAIN 55 69 Framework-2.  
FT DOMAIN 70 76 Complementarity-determining-2.  
FT DOMAIN 77 108 Framework-3.  
FT DOMAIN 109 118 Complementarity-determining-3.  
FT DOMAIN 119 129 Jk1 segment.  
FT DISULFID 43 108 By similarity.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411B560CC14 CRC64;

```
Best Local Similarity 95.4%; Pred. No. 3.4e-47;
Matches 103; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
DB 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIPA 80
QY 61 RFGSGSGTFTLTISLSQSEDFAVYCCQYNNWPR-TFGQGTKEIK 107
DB 81 RFGSGSGTFTLTISLSQSEDFAVYCCQYNNWPPWTFGQGTKEIK 128

RESULT 2
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P01625; 1LVE.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 92.4%; Score 513; DB 2; Length 108;
Best Local Similarity 93.5%; Pred. No. 4.5e-46;
Matches 100; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTISLSQSEDFAVYCCQYNNWPR-TFGQGTKEIK 107
DB 61 RFGSGSGTFTLTISLSQSEDFAVYCCQYNNWPPWTFGQGTKEIK 107

RESULT 3
KV3F HUMAN
ID KV3F HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region POW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```

RN SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive Igm anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma
CC globulin activity.
DR PIR; A01897; K3HUPM.
DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 91.6%; Score 508.5; DB 1; Length 109;
Best Local Similarity 91.7%; Pred. No. 1.3e-45;
Matches 99; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIP 59
DB 1 EIVMTQSPVTLSPGERATLSCRASQSVSNLAWYQQKPGSGRLLIYGASTRATGIP 60
QY 60 ARFSGSGSGTFTLTISLSQSEDFAVYCCQYNNWPR-TFGQGTKEIK 107
DB 61 ARFSGSGSGTFTLTISLSQSEDFAVYCCQYNNWPPWTFGQGTKEIK 108

RESULT 4
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR PIR; D30609; D30609.
DR HSSP; P01625; 1EK3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 91.1%; Score 505.5; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 2.8e-45;
Matches 99; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
```

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
 Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
 QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107  
 Db 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 108

## RESULT 5

Q6GMW0 PRELIMINARY; PRT; 235 AA.  
 AC O6GMW0;  
 DT 05-JUL-2004 (T-REMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-REMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-REMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Fellings E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073792; AAH73792.1; -;  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG cl.  
 DR InterPro; IPR003006; IG\_WHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00409; IG1; 1.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 235 AA; 25765 MW; 4360C36BD4133F5 CRC64;

Query Match 89.3%; Score 495.5; DB 2; Length 235;  
 Best Local Similarity 88.9%; Pred. No. 7.6e-44;  
 Matches 96; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
 Db 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPG 80

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107  
 Db 81 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 128

## RESULT 6

KV3L\_HUMAN STANDARD; PRT; 129 AA.  
 ID KV3L\_HUMAN  
 AC P18135;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region HAH precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88171307; PubMed=3127527;  
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
 RT "Autoantibody-associated kappa light chain variable region gene  
 expressed in chronic lymphocytic leukemia with little or no somatic  
 mutation. Implications for etiology and immunotherapy.";  
 RT J. Exp. Med. 167:840-852(1988).  
 RL -!- DISEASE: The protein is one of the surface immunoglobulin M  
 autoantibodies expressed in patients with chronic lymphocytic  
 leukemia.  
 CC PIR; P10022; K3HUHA.  
 DR HSSP; P01625; 1EQ.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 Ig kappa chain V-III region HAH.  
 FT DOMAIN 21 43 Framework-1.  
 FT DOMAIN 44 55 Complementarity-determining-1.  
 FT DOMAIN 56 70 Framework-2.  
 FT DOMAIN 71 77 Complementarity-determining-2.  
 FT DOMAIN 78 109 Framework-3.  
 FT DOMAIN 110 118 Complementarity-determining-3.  
 FT DOMAIN 119 129 JKI segment.  
 FT DISULFID 43 109 By similarity.  
 FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14073 MW; D3C5292772774D0 CRC64;

Query Match 85.1%; Score 472.5; DB 1; Length 129;  
 Best Local Similarity 86.1%; Pred. No. 9.9e-42;  
 Matches 93; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIP 59  
 Db 21 EIVLTQSPCTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSRATGIP 80

QY 60 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFGQGTKEIK 107  
 Db 81 DRFGSGSGTDTLTISRLEPEDFAVYCCQYGTSPRTFGQGTKEIK 128

## RESULT 7

KV3B\_HUMAN STANDARD; PRT; 109 AA.  
 ID KV3B\_HUMAN  
 AC P01620;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

```
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01892; K3HUI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 84.2%; Score 467.5; DB 1; Length 109;
Best Local Similarity 84.3%; Pred. No. 2.7e-41;
Matches 91; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSN-LAWYQQKPGQAPRLIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSN-LAWYQQKPGQAPRLIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSFSTFGQGTKVELK 108

RESULT 8
KV3D_HUMAN STANDARD; PRT; 109 AA.
ID KV3D_HUMAN
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region fi.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for the
RT mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

Query Match 84.2%; Score 467.5; DB 1; Length 109;
Best Local Similarity 84.3%; Pred. No. 2.7e-41;
Matches 91; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSN-LAWYQQKPGQAPRLIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSN-LAWYQQKPGQAPRLIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSFSTFGQGTKVEIK 108

RESULT 9
KV3E_HUMAN STANDARD; PRT; 109 AA.
ID KV3E_HUMAN
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01896; K3HUI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 83.2%; Score 461.5; DB 1; Length 109;
Best Local Similarity 84.3%; Pred. No. 1.2e-40;
Matches 91; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSN-LAWYQQKPGQAPRLIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSN-LAWYQQKPGQAPRLIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSFSTFGQGTKVELK 108

RESULT 10
KV3F_HUMAN STANDARD; PRT; 109 AA.
ID KV3F_HUMAN
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01897; K3HUI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

Query Match 83.0%; Score 460.5; DB 1; Length 109;
Best Local Similarity 84.3%; Pred. No. 1.5e-40;
Matches 91; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSVSN-LAWYQQKPGQAPRLIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSN-LAWYQQKPGQAPRLIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSFSTFGQGTKVEIK 108

RESULT 10
```

ID	QV3M_HUMAN	STANDARD;	PRT;	129 AA.
AC	P18136;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-III region HIC precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88171307; PubMed=3127527;			
RA	Klapps T.J., Tomhave E., Chen P.P., Carson D.A.;			
RT	"Autoantibody-associated kappa light chain variable region gene			
RT	expressed in chronic lymphocytic leukemia with little or no somatic			
RT	mutation. Implications for etiology and immunotherapy.";			
RL	J. Exp. Med. 167:840-852(1988).			
CC	-1- DISEASE: The protein is one of the surface immunoglobulin M			
CC	autoantibodies expressed in patients with chronic lymphocytic			
CC	leukemia.			
DR	PIR; PL0021; K3HUHI.			
DR	HSSP; P01625; IEEQ.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS0835; IG_LIKE; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL	1	20	
FT	CHAIN	21	129	Ig kappa chain V-III region HIC.
FT	DOMAIN	21	43	Framework-1.
FT	DOMAIN	44	55	Complementarity-determining-1.
FT	DOMAIN	56	70	Framework-2.
FT	DOMAIN	71	77	Complementarity-determining-2.
FT	DOMAIN	78	109	Framework-3.
FT	DOMAIN	110	118	Complementarity-determining-3.
FT	DOMAIN	119	129	JKI segment.
FT	DISULFID	43	109	By similarity.
FT	NON_TER	129	129	
SQ	SEQUENCE	129 AA;	14070 MW;	7395528EA2BB74D6 CRC64;
	Query Match	82.8%;	Score 459.5;	DB 1; Length 129;
	Best Local Similarity	84.3%;	Pred. No. 2.3e-40;	
	Matches	91; Conservative	8; Mismatches	8; Indels 1; Gaps 1;
QY	1	EIVMTQSPATLSVSPGERATLSCRASQSVNN-LAWYQQKPGQAPRLIIYGASTRATGIP	59	
Db	21	EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYVGSSTRATGIP	80	
QY	60	ARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRFTFGQTKVEIK	107	
Db	81	DRFSGSGSGTDFTLTISLRPEXDPFVYYCQYGGSPWTFGQTKVEIK	128	
RESULT 11				
Q9UL78				
ID	Q9UL78	PRELIMINARY;	PRT;	109 AA.
AC	Q9UL78;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Myosin-reactive immunoglobulin light chain variable region			
DE	(Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			

```
DR PIR; A01893; K3HUGO.
DR HSSP; P01625; 1EK3.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;

Query Match 79.7%; Score 442.5; DB 1; Length 109;
Best Local Similarity 80.6%; Pred. No. 1.2e-38;
Matches 87; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSN--LAWYQKPKGQAPRLIIYGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRAALLSRGVLAWYQKPKGQAPRLIIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRTFGGTKVEIK 107
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYGSFPRFGGKVEIK 108

RESULT 13
KV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA PubMed=11946339;
RX Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01891; K3HUB6.
DR HSSP; P01625; 1EEQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 79.2%; Score 439.5; DB 1; Length 108;
Best Local Similarity 76.9%; Pred. No. 2.4e-38;
Matches 83; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSN--LAWYQKPKGQAPRLIIYGASTRATGIP 59
Db 1 ZIVLTSPGTLSPGZRAALSCRAQLSGNVLAWYQKPKGQAPRLIIYGASTRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWPRTFGGTKVEIK 107
Db 61 DRFSGSGSGADFTLTISRLEPEDFAVYVCOQYGSFPRFGGSKLEIK 108

RESULT 14
KV3I_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DR 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Fecht M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated within
the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP; P01625; 1EEQ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 Ig kappa chain V-III region VG.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 54 Complementarity-determining-1.
FT DOMAIN 55 69 Framework-2.
FT DOMAIN 70 76 Complementarity-determining-2.
FT DOMAIN 77 108 Framework-3.
FT DOMAIN 109 115 Complementarity-determining-3.
FT DISULFID 43 108 By similarity.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 78.9%; Score 438; DB 1; Length 115;
Best Local Similarity 88.4%; Pred. No. 3.7e-38;
Matches 84; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSN--LAWYQKPKGQAPRLIIYGASTRATGIP 60
Db 21 EIVLTQSPATLSVSPGERATLSCRASQSVSSYLAWYQKPKGQAPRLIIYDASNRATGIP 80

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNWP 95
Db 81 RFSGSGSGTDFTLTISRLEPEDFAVYVCOQYNNWP 115

RESULT 15
Q6GMV9 PRELIMINARY; PRT; 235 AA.
ID Q6GMV9
AC Q6GMV9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```



DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC073793; AAH73793.1; -  
DR InterPro: IPR003599; Ig-like.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003597; Ig\_c1.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF07654; C1-set; 1.  
DR Pfam: PF00047; ig; 2.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IGc1; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 2.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 78.6%; Score 436.5; DB 2; Length 235;  
Best Local Similarity 80.6%; Pred. No. 1.2e-37;  
Matches 87; Conservative 7; Mismatches 13; Indels 1; Gaps 1;  
QY 1 EIVMTSPATLSVSPGERATLSCRASQSV-SNNLAWYQKPGQAPRLIYGASTRATGIP 59  
DB 21 EIVLTQSPGTLSPGERAALS CRASQSVNSKYLAWYQKPGQAPRLMYAASIRATGIP 80  
QY 60 ARFSGSGSGTEFTLTISSLQSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
DB 81 DRFSGSGSGTDFTLTISRLESEDFALYFCQYGTSPITFGGGTKVEIK 128

Search completed: November 16, 2005, 22:01:50  
Job time : 59.9908 secs

(028) 230 10 000 000

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357A-6  
Perfect score: 555  
Sequence: 1 EIVMTQSPATLSVSPGERAT.....COQYNNWPRTFGQGTKEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529.5	95.4	117	4 US-09-203-768A-4	Sequence 4, Appli
2	498	89.7	224	4 US-09-456-090A-82	Sequence 82, Appl
3	498	89.7	224	4 US-09-456-090A-88	Sequence 88, Appl
4	498	89.7	224	4 US-09-456-090A-90	Sequence 90, Appl
5	498	89.7	224	4 US-09-453-234-82	Sequence 82, Appl
6	498	89.7	224	4 US-09-453-234-88	Sequence 88, Appl
7	498	89.7	224	4 US-09-453-234-90	Sequence 90, Appl
8	495	89.2	224	4 US-09-456-090A-36	Sequence 36, Appl
9	495	89.2	224	4 US-09-453-234-36	Sequence 36, Appl
10	485	87.4	224	4 US-09-456-090A-84	Sequence 84, Appl
11	485	87.4	224	4 US-09-453-234-84	Sequence 84, Appl
12	484	87.2	224	4 US-09-456-090A-46	Sequence 46, Appl
13	484	87.2	224	4 US-09-453-234-46	Sequence 46, Appl
14	475	85.6	106	4 US-08-635-109-8	Sequence 8, Appli
15	475	85.6	106	4 US-08-844-215-11	Sequence 11, Appl
16	471.5	85.0	109	3 US-09-025-769B-16	Sequence 16, Appl
17	471.5	85.0	109	4 US-09-490-070A-16	Sequence 16, Appl
18	471.5	85.0	109	4 US-09-490-153-16	Sequence 16, Appl
19	471.5	85.0	109	4 US-09-490-324-16	Sequence 16, Appl
20	470.5	84.8	110	3 US-09-025-769B-30	Sequence 30, Appl
21	470.5	84.8	110	3 US-09-025-769B-47	Sequence 47, Appl
22	470.5	84.8	110	4 US-09-490-070A-30	Sequence 30, Appl
23	470.5	84.8	110	4 US-09-490-070A-47	Sequence 47, Appl
24	470.5	84.8	110	4 US-09-490-153-30	Sequence 30, Appl
25	470.5	84.8	110	4 US-09-490-153-47	Sequence 47, Appl
26	470.5	84.8	110	4 US-09-490-324-30	Sequence 30, Appl
27	470.5	84.8	110	4 US-09-490-324-47	Sequence 47, Appl

28	467	84.1	234	3 US-09-049-672A-6	Sequence 6, Appli
29	463.5	83.5	108	2 US-08-232-081B-42	Sequence 42, Appl
30	463	83.4	107	4 US-09-438-954-40	Sequence 40, Appl
31	462	83.2	107	1 US-08-107-669D-14	Sequence 14, Appl
32	462	83.2	107	1 US-08-472-788A-14	Sequence 14, Appl
33	462	83.2	107	2 US-08-477-531B-14	Sequence 14, Appl
34	462	83.2	107	2 US-08-082-842A-14	Sequence 14, Appl
35	460.5	83.0	108	1 US-07-634-278-86	Sequence 86, Appl
36	460.5	83.0	108	1 US-08-477-728-86	Sequence 86, Appl
37	460.5	83.0	108	1 US-08-474-040-86	Sequence 86, Appl
38	460.5	83.0	108	1 US-08-487-200-86	Sequence 86, Appl
39	460.5	83.0	108	1 US-08-488-113B-150	Sequence 150, App
40	460.5	83.0	108	1 US-08-477-484B-150	Sequence 150, App
41	460.5	83.0	108	2 US-08-646-360-150	Sequence 150, App
42	460.5	83.0	108	3 US-08-839-765-150	Sequence 150, App
43	460.5	83.0	108	3 US-09-136-389-150	Sequence 150, App
44	460.5	83.0	108	3 US-08-484-537-86	Sequence 86, Appl
45	460.5	83.0	108	3 US-09-610-838-150	Sequence 150, App

ALIGNMENTS

RESULT 1  
US-09-203-768A-4  
; Sequence 4, Application US/09203768A  
; Patent No. 6787638  
; GENERAL INFORMATION:  
; APPLICANT: Huse, William D.  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods  
; FILE REFERENCE: P-IX 2947  
; CURRENT APPLICATION NUMBER: US/09/203,768A  
; CURRENT FILING DATE: 1998-12-02  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-203-768A-4

Query Match	95.4%	Score	529.5	DB	4	Length	117
Best Local Similarity	96.3%	Pred. No.	3.8e-40				
Matches	104	Conservative	2	Mismatches	1	Indels	1
						Gaps	1
QY	1	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA	60				
DB	9	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA	68				
QY	61	RFGSGSGTFTLTITSSLSQSEDFAVYCCQYNNW-PRTEGQGTKEIK	107				
DB	69	RFGSGSGTFTLTITSSLSQSEDFAVYCCQYNNWPPYTFGQGTKEIK	116				

RESULT 2  
US-09-456-090A-82  
; Sequence 82, Application US/09456090A  
; Patent No. 6680209  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS  
; FILE REFERENCE: 020015-00020005  
; CURRENT APPLICATION NUMBER: US/09/456,090A  
; CURRENT FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 224

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDFLTITISLSEPFDAVYYCQORTNWPRTFGGTKVEIK 107

RESULT 3
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDFLTITISLSEPFDAVYYCQORTNWPRTFGGTKVEIK 107

RESULT 4
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDFLTITISLSEPFDAVYYCQORTNWPRTFGGTKVEIK 107

RESULT 5
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDFLTITISLSEPFDAVYYCQORTNWPRTFGGTKVEIK 107

RESULT 6
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
US-09-453-234-88
```

```
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-453-234-88

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAHYQOKPGQAPRLIIYDASNRTATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFQGGTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLSPEDFAVYYCQQRNWPRTFQGGTKVEIK 107

RESULT 7
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match      89.7%; Score 498; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAHYQOKPGQAPRLIIYDASNRTATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFQGGTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLSPEDFAVYYCQQRNWPRTFQGGTKVEIK 107

RESULT 8
US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-1L
US-09-456-090A-36

Query Match      89.2%; Score 495; DB 4; Length 224;
Best Local Similarity 88.8%; Pred. No. 8.9e-37;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAHYQOKPGQAPRLIIYDASNRTATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFQGGTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLSPEDFAVYYCQQRNWPRTFQGGTKVEIK 107

RESULT 9
US-09-453-234-36
; Sequence 36, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-36

Query Match      89.2%; Score 495; DB 4; Length 224;
Best Local Similarity 88.8%; Pred. No. 8.9e-37;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAHYQOKPGQAPRLIIYDASNRTATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFQGGTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLSPEDFAVYYCQQRNWPRTFQGGTKVEIK 107

RESULT 10
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
```

; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 84  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M2-32L  
US-09-456-090A-84

Query Match 87.4%; Score 485; DB 4; Length 224;  
Best Local Similarity 87.9%; Pred. No. 6.9e-36;  
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
Db 1 EIVLTQSPATLSVSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRAAGIPA 60  
QY 61 RFGSGSGTFTLTISLSLOSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
Db 61 RFGSGSGTFTLTISLSLEPEDFAVYCCQYNNWPLTFGGTKVEIK 107

## RESULT 11

US-09-453-234-84  
; Sequence 84, Application US/09453234  
; Patent No. 6794132  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Walkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: US 60/157,415  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 84  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M2-32L  
US-09-453-234-84

Query Match 87.4%; Score 485; DB 4; Length 224;  
Best Local Similarity 87.9%; Pred. No. 6.9e-36;  
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
Db 1 EIVLTQSPATLSVSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRAAGIPA 60  
QY 61 RFGSGSGTFTLTISLSLOSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
Db 61 RFGSGSGTFTLTISLSLEPEDFAVYCCQYNNWPLTFGGTKVEIK 107

## RESULT 12

US-09-456-090A-46  
; Sequence 46, Application US/09456090A  
; Patent No. 6680209  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Walkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS  
; FILE REFERENCE: 020015-000200US  
; CURRENT APPLICATION NUMBER: US/09/456,090A

; CURRENT FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-10L  
US-09-456-090A-46

Query Match 87.2%; Score 484; DB 4; Length 224;  
Best Local Similarity 86.9%; Pred. No. 8.5e-36;  
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
Db 1 DVVMTQSPATLSVSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRAATGIPA 60  
QY 61 RFGSGSGTFTLTISLSLOSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
Db 61 RFGSGSGTFTLTISLSLEPEDFAVYCCQYNNWPRTFGGTKVEIK 107

## RESULT 13

US-09-453-234-46  
; Sequence 46, Application US/09453234  
; Patent No. 6794132  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Walkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: US 60/157,415  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-10L  
US-09-453-234-46

Query Match 87.2%; Score 484; DB 4; Length 224;  
Best Local Similarity 86.9%; Pred. No. 8.5e-36;  
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
Db 1 DVVMTQSPATLSVSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRAATGIPA 60  
QY 61 RFGSGSGTFTLTISLSLOSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
Db 61 RFGSGSGTFTLTISLSLEPEDFAVYCCQYNNWPRTFGGTKVEIK 107

## RESULT 14

US-08-635-109-8  
; Sequence 8, Application US/08635109  
; Patent No. 6538114  
; GENERAL INFORMATION:  
; APPLICANT: Persson, Mats A. A.  
; APPLICANT: Allander, Tobias E.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:



(CAND) 11/12/2011



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds  
(without alignments)  
681.481 Million cell updates/sec

Title: US-10-660-357A-6  
Perfect score: 555  
Sequence: 1 EIVMTQSPATLSVSPGERAT.....COQYNNWPRTFCQGTKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA.\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	107	14	US-10-330-613-6
2	555	100.0	107	14	US-10-330-530-6
3	555	100.0	107	16	US-10-660-357-6
4	546	98.4	107	14	US-10-330-613-34
5	546	98.4	107	14	US-10-330-530-34
6	546	98.4	107	16	US-10-660-357-34
7	543	97.8	107	15	US-10-251-085B-122
8	543	97.8	107	16	US-10-737-252-122
9	539	97.1	107	15	US-10-251-085B-126
10	539	97.1	107	16	US-10-737-252-126
11	536	96.6	107	15	US-10-251-085B-109
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 34, Appl
					Sequence 34, Appl
					Sequence 122, App
					Sequence 126, App
					Sequence 126, App
					Sequence 109, App

12	536	96.6	107	15	US-10-251-085B-123	Sequence 123, App
13	536	96.6	107	16	US-10-737-252-109	Sequence 109, App
14	536	96.6	107	16	US-10-737-252-123	Sequence 123, App
15	536	96.6	107	17	US-10-727-155-310	Sequence 310, App
16	536	96.6	107	17	US-10-727-155-313	Sequence 313, App
17	536	96.6	107	18	US-10-901-736-2	Sequence 2, Appli
18	534	96.2	107	15	US-10-251-085B-117	Sequence 117, App
19	534	96.2	107	16	US-10-737-252-117	Sequence 117, App
20	533.5	96.1	108	15	US-10-251-085B-132	Sequence 132, App
21	533.5	96.1	108	16	US-10-737-252-132	Sequence 132, App
22	533	96.0	107	15	US-10-251-085B-119	Sequence 119, App
23	533	96.0	107	16	US-10-737-252-119	Sequence 119, App
24	533	96.0	107	17	US-10-727-155-314	Sequence 314, App
25	533	96.0	107	17	US-10-938-353-107	Sequence 107, App
26	532.5	95.9	108	18	US-10-984-960A-29	Sequence 29, Appl
27	532	95.9	250	10	US-09-880-748-1952	Sequence 1952, Ap
28	532	95.9	250	15	US-10-293-418-1952	Sequence 1952, Ap
29	529.5	95.4	117	14	US-10-300-675-4	Sequence 4, Appli
30	529.5	95.4	117	14	US-10-300-675-42	Sequence 42, Appl
31	529.5	95.4	117	14	US-10-300-675-44	Sequence 44, Appl
32	529.5	95.4	117	14	US-10-300-675-46	Sequence 46, Appl
33	529.5	95.4	117	17	US-10-910-124-4	Sequence 4, Appli
34	529	95.3	246	10	US-09-880-748-1268	Sequence 1268, Ap
35	529	95.3	246	15	US-10-293-418-1268	Sequence 1268, Ap
36	528	95.1	107	15	US-10-251-085B-115	Sequence 115, App
37	528	95.1	107	16	US-10-737-252-115	Sequence 115, App
38	526	94.8	107	15	US-10-308-817-124	Sequence 124, App
39	526	94.8	107	15	US-10-453-698-124	Sequence 124, App
40	525	94.6	107	17	US-10-727-155-146	Sequence 146, App
41	525	94.6	107	17	US-10-727-155-184	Sequence 184, App
42	525	94.6	127	15	US-10-309-764-137	Sequence 137, App
43	524.5	94.5	106	17	US-10-727-155-277	Sequence 277, App
44	524	94.4	154	16	US-10-665-383-82	Sequence 82, Appl
45	523.5	94.3	108	17	US-10-893-576-182	Sequence 182, App

ALIGNMENTS

RESULT 1  
US-10-330-613-6  
; Sequence 6, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX 022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-6

Query Match 100.0%; Score 555; DB 14; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2.9e-40;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA	60
Db	1	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA	60
Qy	61	RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFCQGTKVEIK	107
Db	61	RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFCQGTKVEIK	107

RESULT 2

```
US-10-330-530-6
; Sequence 6, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX 031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-6

Query Match      100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 3
US-10-660-357-6
; Sequence 6, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX 030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-6

Query Match      100.0%; Score 555; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 4
US-10-330-613-34
; Sequence 34, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
```

```
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-34

Query Match      98.4%; Score 546; DB 14; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.7e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 5
US-10-330-530-34
; Sequence 34, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX 031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-34

Query Match      98.4%; Score 546; DB 14; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.7e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 6
US-10-660-357-34
; Sequence 34, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX 030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
```

; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-660-357-34

Query Match 98.4%; Score 546; DB 16; Length 107;  
Best Local Similarity 97.2%; Pred. No. 1.7e-39;  
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
|||||  
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
|||||

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107  
|||||

DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107  
|||||

## RESULT 7

US-10-251-085B-122

; Sequence 122, Application US/10251085B  
; Publication No. US20040072164A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; APPLICANT: Lin, Ying-Chi  
; APPLICANT: Maruyama, Toshiaki  
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION  
; FILE REFERENCE: 1087-21  
; CURRENT APPLICATION NUMBER: US/10/251,085B  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: US 60/323,455  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 122  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: human  
US-10-251-085B-122

Query Match 97.8%; Score 543; DB 15; Length 107;  
Best Local Similarity 98.1%; Pred. No. 3.1e-39;  
Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
|||||  
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
|||||

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107  
|||||

DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107  
|||||

## RESULT 8

US-10-737-252-122

; Sequence 122, Application US/10737252  
; Publication No. US20040175736A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; APPLICANT: Lin, Ying-Chi  
; APPLICANT: Maruyama, Toshiaki  
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION  
; FILE REFERENCE: 1087-21 CIP  
; CURRENT APPLICATION NUMBER: US/10/737,252  
; CURRENT FILING DATE: 2003-12-15

; PRIOR APPLICATION NUMBER: US 10/251,085  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: US 60/323,455  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 122  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: human  
US-10-737-252-122

Query Match 97.8%; Score 543; DB 16; Length 107;  
Best Local Similarity 98.1%; Pred. No. 3.1e-39;  
Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
|||||

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
|||||

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107  
|||||

DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107  
|||||

## RESULT 9

US-10-251-085B-126

; Sequence 126, Application US/10251085B  
; Publication No. US20040072164A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; APPLICANT: Lin, Ying-Chi  
; APPLICANT: Maruyama, Toshiaki  
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION  
; FILE REFERENCE: 1087-21  
; CURRENT APPLICATION NUMBER: US/10/251,085B  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: US 60/323,455  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 126  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: human  
US-10-251-085B-126

Query Match 97.1%; Score 539; DB 15; Length 107;  
Best Local Similarity 97.2%; Pred. No. 6.8e-39;  
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
|||||

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
|||||

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107  
|||||

DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWPRTFGQGTKVEIK 107  
|||||

## RESULT 10

US-10-737-252-126

; Sequence 126, Application US/10737252  
; Publication No. US20040175736A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; APPLICANT: Lin, Ying-Chi  
; APPLICANT: Maruyama, Toshiaki  
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION

; FILE REFERENCE: 1087-21 CIP  
; CURRENT APPLICATION NUMBER: US/10/737,252  
; CURRENT FILING DATE: 2003-12-15  
; PRIOR APPLICATION NUMBER: US 10/251,085  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: US 60/323,455  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 126  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: human  
US-10-737-252-126

Query Match 97.1%; Score 539; DB 16; Length 107;  
Best Local Similarity 97.2%; Pred. No. 6.8e-39;  
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60  
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGTSTRATGIPA 60  
  
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107  
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107

RESULT 11  
US-10-251-085B-109  
; Sequence 109, Application US/10251085B  
; Publication No. US20040072164A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; APPLICANT: Lin, Ying-Chi  
; APPLICANT: Maruyama, Toshiaki  
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION  
; FILE REFERENCE: 1087-21  
; CURRENT APPLICATION NUMBER: US/10/251,085B  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: US 60/323,455  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 109  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: human  
US-10-251-085B-109

Query Match 96.6%; Score 536; DB 15; Length 107;  
Best Local Similarity 96.3%; Pred. No. 1.2e-38;  
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60  
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGTSTRATGIPA 60  
  
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107  
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107

RESULT 12  
US-10-251-085B-123  
; Sequence 123, Application US/10251085B  
; Publication No. US20040072164A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark

; APPLICANT: Lin, Ying-Chi  
; APPLICANT: Maruyama, Toshiaki  
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION  
; FILE REFERENCE: 1087-21  
; CURRENT APPLICATION NUMBER: US/10/251,085B  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: US 60/323,455  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 123  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: human  
US-10-251-085B-123

Query Match 96.6%; Score 536; DB 15; Length 107;  
Best Local Similarity 96.3%; Pred. No. 1.2e-38;  
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60  
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGTSTRATGIPA 60  
  
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107  
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107

RESULT 13  
US-10-737-252-109  
; Sequence 109, Application US/10737252  
; Publication No. US20040175736A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; APPLICANT: Lin, Ying-Chi  
; APPLICANT: Maruyama, Toshiaki  
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION  
; FILE REFERENCE: 1087-21 CIP  
; CURRENT APPLICATION NUMBER: US/10/737,252  
; CURRENT FILING DATE: 2003-12-15  
; PRIOR APPLICATION NUMBER: US 10/251,085  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: US 60/323,455  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 109  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: human  
US-10-737-252-109

Query Match 96.6%; Score 536; DB 16; Length 107;  
Best Local Similarity 96.3%; Pred. No. 1.2e-38;  
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60  
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGTSTRATGIPA 60  
  
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107  
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107

RESULT 14  
US-10-737-252-123  
; Sequence 123, Application US/10737252  
; Publication No. US20040175736A1  
; GENERAL INFORMATION:

APPLICANT: Bowdish, Katherine S.  
APPLICANT: Frederickson, Shana  
APPLICANT: Renshaw, Mark  
APPLICANT: Lin, Ying-Chi  
APPLICANT: Mariyama, Toshiaki  
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION  
FILE REFERENCE: 1087-21 CIP  
CURRENT APPLICATION NUMBER: US/10/737,252  
CURRENT FILING DATE: 2003-12-15  
PRIOR APPLICATION NUMBER: US 10/251,085  
PRIOR FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: US 60/323,455  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 309  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 123  
LENGTH: 107  
TYPE: PRT  
ORGANISM: human  
US-10-737-252-123

Query Match 96.6%; Score 536; DB 16; Length 107;  
Best Local Similarity 96.3%; Pred. No. 1.2e-38;  
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
QY 61 RFGSGSGTTEFTLTITSSLOSEDFAVYVCOQYNNWPTFGQGTKEIK 107  
DB 61 RFGSGSGTTEFTLTITSSLOSEDFAVYVCOQYNNWPTFGQGTKEIK 107

RESULT 15  
US-10-727-155-310  
Sequence 310, Application US/10727155  
Publication No. US20050049402A1  
GENERAL INFORMATION:  
APPLICANT: John S. Babcock  
APPLICANT: Jaspal S. Kang  
APPLICANT: Orit Foord  
APPLICANT: Larry Green  
APPLICANT: Xiao Feng  
APPLICANT: Scott Klakamp  
APPLICANT: Mary Haak-Frendscho  
APPLICANT: Palaniswami Rathanaswami  
APPLICANT: Craig Pigott  
APPLICANT: Meina Liang  
APPLICANT: Rozanne Lee  
APPLICANT: Kathy Manchulenchao  
APPLICANT: Raffaela Faggioni  
APPLICANT: Giorgio Senaldi  
APPLICANT: Qiaojuan Jane Su  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
FILE REFERENCE: ABGENIX.073A  
CURRENT APPLICATION NUMBER: US/10/727,155  
CURRENT FILING DATE: 2003-12-02  
PRIOR APPLICATION NUMBER: 60/430729  
PRIOR FILING DATE: 2002-12-02  
NUMBER OF SEQ ID NOS: 320  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 310  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-727-155-310

Query Match 96.6%; Score 536; DB 17; Length 107;  
Best Local Similarity 96.3%; Pred. No. 1.2e-38;  
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIIYGASTRATGIPA 60  
QY 61 RFGSGSGTTEFTLTITSSLOSEDFAVYVCOQYNNWPTFGQGTKEIK 107  
DB 61 RFGSGSGTTEFTLTITSSLOSEDFAVYVCOQYNNWPTFGQGTKEIK 107

Search completed: November 16, 2005, 23:05:40  
Job time : 66.6949 secs

(C) 2000 Xerox Corporation

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 62.5147 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-10  
Perfect score: 566  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QSYSTPPESFGQTKLEIK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	566	100.0	109	7	Adc99781 Anti-huma
2	566	100.0	109	7	Add05385 Anti-MUC1
3	566	100.0	109	7	Adf09823 Human ant
4	520	91.9	108	8	Adp47299 Human pho
5	520	91.9	214	8	Adr23360 Human CD7
6	520	91.9	214	8	Adr23358 Human CD7
7	520	91.9	214	8	Adr23366 Human CD7
8	520	91.9	214	8	Adr23364 Human CD7
9	519.5	91.8	237	3	Aay96298 Human IGF
10	519	91.7	108	8	Adp47103 Human pho
11	517	91.3	108	8	Adp47113 Human pho
12	515.5	91.1	237	3	Aay96289 Human IGF
13	512	90.5	107	8	Adp22402 Human ant
14	512	90.5	108	8	Adp47294 Human pho
15	512	90.5	132	2	AAW22842 Human ant
16	511	90.3	106	8	Adr47411 Human ger
17	511	90.3	108	6	Abp96009 HSA antib
18	511	90.3	108	8	Adl92386 Anti-RSA
19	511	90.3	108	8	Adq14601 Single-o
20	511	90.3	108	8	Adq77191 Dummy vk
21	511	90.3	108	8	Adq77181 VK dummy
22	511	90.3	108	8	Adg90912 Vk/Ck pro
23	511	90.3	108	8	AdS78333 vkappa du
24	511	90.3	108	8	AdS78331 Dkappa9-
25	511	90.3	240	2	Aay02472 A single

26	511	90.3	240	4	AAB46007	Aab46007 Human MUC
27	511	90.3	240	4	AAB46038	Aab46038 Human TF
28	511	90.3	240	4	AAB46008	Aab46008 Human MUC
29	511	90.3	240	4	AAB46006	Aab46006 Human MUC
30	511	90.3	240	4	AAB46005	Aab46005 Human MUC
31	511	90.3	240	6	ABP95997	Abp95997 Human ser
32	511	90.3	240	8	ADL92369	Adl92369 Human pha
33	511	90.3	240	8	ADQ77165	Adq77165 HSA Heavy
34	510	90.1	249	8	ADR23322	Adr23322 Human CD7
35	510	90.1	249	8	ADR23326	Adr23326 Human CD7
36	509	89.9	108	6	AAO16706	Aao16706 Human ant
37	509	89.9	108	8	ADP47107	Adp47107 Human pho
38	508.5	89.8	111	8	ADP47305	Adp47305 Human pho
39	506	89.4	107	2	AAW16649	Aaw16649 Anti-canc
40	505.5	89.3	108	4	AAG93589	Aag93589 Human ant
41	505.5	89.3	108	4	AAG93600	Aag93600 Human ant
42	505.5	89.3	108	6	ABO27407	Abo27407 Anti-Rh(D
43	505.5	89.3	108	6	ABO27396	Abo27396 Anti-Rh(D
44	505.5	89.3	111	8	ADP47306	Adp47306 Human pho
45	505	89.2	107	4	AAG65567	Aag65567 Amino ac1

ALIGNMENTS

RESULT 1  
ADC99781  
ID ADC99781 standard; protein; 109 AA.  
XX  
AC ADC99781;  
XX

01-JAN-2004 (first entry)

Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 10.

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
lung cancer; human.

Homo sapiens.

WO2003057838-A2.

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P.

(ABGE-) ABGENIX INC.

Gudas J;

WPI; 2003-587113/55.

N-PSDB; ADC99783.

New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

Claim 3; SEQ ID NO 10; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

```
CC light chain protein of the invention.
XX
SQ Sequence 109 AA;

Query Match      100.0%; Score 566; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 9e-33;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109

RESULT 2
ADD05385
ID ADD05385 standard; protein; 109 AA.
XX
AC ADD05385;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 10.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
WPI; 2003-577496/54.
DR N-PSDB; ADD05387.
XX

Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
Claim 3; SEQ ID NO 10; 87pp; English.
XX
The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
SQ Sequence 109 AA;

Query Match      100.0%; Score 566; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 9e-33;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109

RESULT 3
ADF09823
ID ADF09823 standard; protein; 109 AA.
XX
AC ADF09823;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #3.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI; 2003-598367/56.
DR N-PSDB; ADF09825.
XX

Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
Claim 3; SEQ ID NO 10; 83pp; English.
XX
The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 109 AA;

Query Match      100.0%; Score 566; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 9e-33;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTITCRASQSIISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109
```



## RESULT 4

ADP47299  
 ID ADP47299 standard; protein; 108 AA.  
 AC  
 ADP47299;  
 AC  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human phospholipase A2-specific monoclonal antibody light chain #19.  
 XX  
 DE human; monoclonal antibody; phospholipase A2; PLA2;  
 KW inflammatory disorder; degenerative disorder;  
 KW joint inflammatory reaction; skin inflammatory reaction;  
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;  
 KW Alzheimer's disease; atherosclerosis; restenosis; light chain.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004050850-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038234.  
 XX  
 PR 02-DEC-2002; 2002US-0430724P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;  
 PI Jia X, Nocerini MR;  
 XX  
 XX WPI; 2004-461119/43.  
 XX

XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),  
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,  
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.  
 XX

PS Example 5; SEQ ID NO 214; 128pp; English.

XX The invention comprises a human monoclonal antibody that binds to  
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is  
 CC useful in the preparation of a medicament for the treatment of  
 CC inflammatory and degenerative disorders stemming from inflammatory  
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,  
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present  
 CC amino acid sequence represents the light chain from a monoclonal antibody  
 CC that is specific for the human phospholipase A2 (PLA2) enzyme.

XX Sequence 108 AA;

Query Match 91.9%; Score 520; DB 8; Length 108;  
 Best Local Similarity 93.6%; Pred. No. 1.6e-29;  
 Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60  
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFTLTISSLPEDFATYYCQSYSTPPCECFGQGTKEIK 109  
 DB 61 RFGSGSGTDFTLTISSLPEDFATYYCQSYSTPP--TFGQGTKEIK 107

## RESULT 5

ADR23360  
 ID ADR23360 standard; protein; 214 AA.  
 XX  
 AC ADR23360;  
 XX  
 DT 04-NOV-2004 (first entry)

XX Human CD72-targeted IgG1 light chain.  
 DE  
 XX

KW Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;  
 KW immunosuppressive; cancer; autoimmune disease; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..108

FT /label= V\_region

FT Region 109..214

FT /label= C\_region

XX WO2004067569-A1.

PN 12-AUG-2004.

XX 27-JAN-2003; 2003WO-EP050004.

XX 27-JAN-2003; 2003WO-EP050004.

PR (CRUC-) CRUCELL HOLLAND BV.

XX Bakker ABH, Marissen WE;

XX WPI; 2004-580978/56.

XX N-PSDB; ADR23359.

XX New internalizing human binding molecules capable of specifically binding  
 to CD72, useful for diagnosing and/or treating B-cell associated  
 diseases, such as cancer or autoimmune disorders.  
 XX  
 PS Example 5; SEQ ID NO 52; 174pp; English.

XX The present sequence is the protein sequence of the light chain of human

CC IgG1 antibody 024, which specifically recognises human B cell associated  
 CC antigen CD72. An scFv ADR23322 selected from an antibody phage display  
 CC library was shown to specifically recognise the human CD72 receptor. The  
 CC scFv was recloned in IGG expression vector C01 using primers designed to  
 CC restore complete human frameworks, thereby generating antibody 024. Such  
 CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used  
 CC as internalising human binding molecules of the invention. These  
 CC internalising human binding molecules are capable of (specifically)  
 CC binding to CD72 or its antigenic determinant, and preferably bind to CD72  
 CC associated with cells. Upon binding to CD72 present on the surface of  
 CC target cells, the binding molecules internalise. In addition to the  
 CC internalising human binding molecules, the invention provides  
 CC immunoconjugates comprising an internalising human binding molecule and a  
 CC tag (toxic substance, radioactive substance, liposome and/or enzyme),  
 CC nucleic acids encoding these, and compositions comprising them. The  
 CC internalising human binding molecule, immunoconjugate, nucleic acid  
 CC molecule or composition can be used in the diagnosis and/or treatment of  
 CC a B cell associated disorder or disease, especially a B cell associated  
 CC cancer and B cell associated autoimmune disorder (claimed).

XX Sequence 214 AA;

Query Match 91.9%; Score 520; DB 8; Length 214;  
 Best Local Similarity 93.6%; Pred. No. 2.9e-29;  
 Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60  
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFTLTISSLPEDFATYYCQSYSTPPCECFGQGTKEIK 109  
 DB 61 RFGSGSGTDFTLTISSLPEDFATYYCQSYSTPP--TFGQGTKEIK 107

RESULT 6  
 ADR23358



Db 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASLSQSGVPS 60  
QY 61 RFSGSGSGTDFTLTISSLQPEDPATYVCROSYSTPPSCSFQGTKEIK 109  
Db 61 RFSGSGSGTDFTLTISSLQPEDPATYVCROSYSTPP--TFGQGTKVEIK 107

RESULT 8  
ADR23364  
ID ADR23364 standard; protein; 214 AA.

XX ADR23364;

XX 04-NOV-2004 (first entry)

XX Human CD72-targeted IgG1 light chain.

XX Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;  
KW immunosuppressive; cancer; autoimmune disease; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..108

FT /label= V\_region

FT 109..214

FT /label= C\_region

XX WO2004067569-A1.

XX 12-AUG-2004.

XX 27-JAN-2003; 2003WO-EP050004.

XX 27-JAN-2003; 2003WO-EP050004.

XX (CRUC-) CRUCELL HOLLAND BV.

XX Bakker ABH, Marissen WE;

XX WPI; 2004-580978/56.

XX N-PSDB; ADR23363.

XX New internalizing human binding molecules capable of specifically binding  
PT to CD72, useful for diagnosing and/or treating B-cell associated  
PT diseases, such as cancer or autoimmune disorders.

XX Example 5; SEQ ID NO 56; 174pp; English.

XX The present sequence is the protein sequence of the light chain of human  
CC IgG1 antibody 041, which specifically recognises human B cell associated  
CC antigen CD72. An scFv ADR23330 selected from an antibody phage display  
CC library was shown to specifically recognise the human CD72 receptor. The  
CC scFv was recloned in IgG expression vector C01 using primers designed to  
CC restore complete human frameworks, thereby generating antibody 041. Such  
CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used  
CC as internalising human binding molecules of the invention. These  
CC internalising human binding molecules are capable of (specifically)  
CC binding to CD72 or its antigenic determinant, and preferably bind to CD72  
CC associated with cells. Upon binding to CD72 present on the surface of  
CC target cells, the binding molecules internalise. In addition to the  
CC internalising human binding molecules, the invention provides  
CC immunocjugates comprising an internalising human binding molecule and a  
CC tag (toxic substance, radioactive substance, liposome and/or enzyme),  
CC nucleic acids encoding these, and compositions comprising them. The  
CC internalising human binding molecule, immunocjugate, nucleic acid  
CC molecule or composition can be used in the diagnosis and/or treatment of  
CC a B cell associated disorder or disease, especially a B cell associated  
CC cancer and B cell associated autoimmune disorder (claimed).

XX Sequence 214 AA;

Query Match 91.9%; Score 520; DB 8; Length 214;  
Best Local Similarity 93.6%; Pred. No. 2.9e-29;  
Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASLSQSGVPS 60

QY 61 RFSGSGSGTDFTLTISSLQPEDPATYVCROSYSTPPSCSFQGTKEIK 109

Db 61 RFSGSGSGTDFTLTISSLQPEDPATYVCROSYSTPP--TFGQGTKVEIK 107

RESULT 9

AAAY96298

ID AAY96298 standard; protein; 237 AA.

XX AAY96298;

XX 16-AUG-2000 (first entry)

XX Human IGFAM-10 immunoglobulin.

XX Human; immunoglobulin; IGFAM-10; IGFAM; immune disorder; cancer;  
KW infection; inflammation; haematopoiesis; AIDS; allergy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..22

FT /label= signal\_peptide

FT Protein 23..237

FT /label= IGFAM-10

FT Domain 38..112

FT /label= Ig\_domain

FT Domain 150..219

FT /label= Ig\_domain

FT Domain 193..236

FT /label= Ig\_domain

XX WO200029583-A2.

XX 25-MAY-2000.

XX 19-NOV-1999; 99WO-US027566.

XX 19-NOV-1998; 98US-00195853.

XX 22-DEC-1998; 98US-0113635P.

XX 07-APR-1999; 99US-0128194P.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;

XX Lu DM, Lal P, Hillman JL, Yang J;

XX WPI; 2000-387796/33.

XX N-PSDB; AAA27390.

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the  
PT protein is useful for preventing and treating disorders associated with  
PT altered levels of the protein such as cancer, immune system disorders.

XX Claim 1; Page 85-86; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein  
CC IGFAM-10. Its gene was isolated from a cDNA library of colon tissue. It  
CC is expressed in reproductive, gastrointestinal and cardiovascular tissue,  
CC where cancer and inflammation are common. The gene, protein, its  
CC antibodies, agonists and antagonists are suitable for diagnosing and  
CC treating many diseases, including cancer, immune system disorders (such  
CC as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma,  
CC atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus,  
CC emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis,

CC rheumatoid arthritis, scleroderma, systemic lupus erythematosus and  
 CC ulcerative colitis), complications of cancer, haemodialysis and  
 CC extracorporeal circulation, trauma and haematopoietic cancer (such as  
 CC leukaemia) and infections caused by bacteria, viruses, fungi or parasites  
 XX  
 SQ Sequence 237 AA;

Query Match 91.8%; Score 519.5; DB 3; Length 237;  
 Best Local Similarity 93.6%; Pred. No. 3.4e-29;  
 Matches 102; Conservative 4; Mismatches 2; Indels 1; Gaps 1;  
 Qy 1 DIQWTSPPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60  
 Db 23 DIQWTSPPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 82  
 Qy 61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPSCSFQGGTKLEIK 109  
 Db 83 RFSGSGSGTDFTLTISSLOPEDFATYYCQOSYSTPP-ITFGQGTKEIK 130

RESULT 10  
 ADP47103  
 ID ADP47103 standard; protein; 108 AA.  
 AC ADP47103;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human phospholipase A2-specific monoclonal antibody light chain #8.

XX human; monoclonal antibody; phospholipase A2; PLA2;  
 KW inflammatory disorder; degenerative disorder;  
 KW joint inflammatory reaction; skin inflammatory reaction;  
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;  
 KW Alzheimer's disease; atherosclerosis; restenosis; light chain.  
 XX  
 OS Homo sapiens.

XX WO2004050850-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038234.  
 XX  
 PR 02-DEC-2002; 2002US-0430724P.

XX (ABGE-) ABGENIX INC.  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;  
 PI Jia X, Nocerini MR;  
 XX WPI; 2004-461119/43.

XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),  
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,  
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.  
 XX  
 PS Claim 2; SEQ ID NO 18; 128pp; English.

XX The invention comprises a human monoclonal antibody that binds to  
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is  
 CC useful in the preparation of a medicament for the treatment of  
 CC inflammatory and degenerative disorders stemming from inflammatory  
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,  
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present  
 CC amino acid sequence represents the light chain from a monoclonal antibody  
 CC that is specific for the human phospholipase A2 (PLA2) enzyme.

XX Sequence 108 AA;  
 Query Match 91.7%; Score 519; DB 8; Length 108;  
 Best Local Similarity 93.6%; Pred. No. 1.8e-29;

Matches 102; Conservative 3; Mismatches 2; Indels 2; Gaps 1;  
 Qy 1 DIQWTSPPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60  
 Db 1 DIQWTSPPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 60  
 Qy 61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPSCSFQGGTKLEIK 109  
 Db 61 RFSGSGSGTDFTLTISSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

RESULT 11  
 ADP47113  
 ID ADP47113 standard; protein; 108 AA.

XX ADP47113;  
 AC  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human phospholipase A2-specific monoclonal antibody light chain #13.  
 XX human; monoclonal antibody; phospholipase A2; PLA2;  
 KW inflammatory disorder; degenerative disorder;  
 KW joint inflammatory reaction; skin inflammatory reaction;  
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;  
 KW Alzheimer's disease; atherosclerosis; restenosis; light chain.  
 XX  
 OS Homo sapiens.

XX WO2004050850-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038234.  
 XX  
 PR 02-DEC-2002; 2002US-0430724P.

XX (ABGE-) ABGENIX INC.  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;  
 PI Jia X, Nocerini MR;  
 XX WPI; 2004-461119/43.

XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),  
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,  
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.  
 XX  
 PS Claim 2; SEQ ID NO 28; 128pp; English.

XX The invention comprises a human monoclonal antibody that binds to  
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is  
 CC useful in the preparation of a medicament for the treatment of  
 CC inflammatory and degenerative disorders stemming from inflammatory  
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,  
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present  
 CC amino acid sequence represents the light chain from a monoclonal antibody  
 CC that is specific for the human phospholipase A2 (PLA2) enzyme.

XX Sequence 108 AA;  
 Query Match 91.3%; Score 517; DB 8; Length 108;  
 Best Local Similarity 92.7%; Pred. No. 2.6e-29;  
 Matches 101; Conservative 5; Mismatches 1; Indels 2; Gaps 1;

Qy 1 DIQWTSPPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60  
 Db 1 DIQWTSPPSSLSASVGDRTTITCRASQISNYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 60  
 Qy 61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPSCSFQGGTKLEIK 109  
 Db 61 RFSGSGSGTDFTLTISSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

RESULT 12  
 AAY96289 ID AAY96289 standard; protein; 237 AA.  
 XX  
 AC AAY96289;  
 XX  
 DT 16-AUG-2000 (first entry)  
 XX  
 DE Human IGFAM-1 immunoglobulin.  
 XX  
 KW Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer;  
 KW infection; inflammation; haematopoiesis; AIDS; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /label= signal\_peptide  
 FT Protein 23..237  
 FT /label= IGFAM-1  
 FT Domain 38..112  
 FT /label= Ig\_domain  
 FT Domain 150..219  
 FT /label= Ig\_domain  
 FT Region 154..176  
 FT /label= Ig\_signature  
 FT Domain 193..236  
 FT /label= Ig\_domain  
 FT Region 215..232  
 FT /label= Ig\_signature  
 XX  
 XX WO200029583-A2.  
 XX  
 XX 25-MAY-2000.  
 XX  
 XX 19-NOV-1999; 99WO-US027566.  
 XX  
 XX 19-NOV-1998; 98US-00195853.  
 PR  
 XX 22-DEC-1998; 98US-0113635P.  
 PR  
 XX 07-APR-1999; 99US-0128194P.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 XX  
 XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;  
 PI Lu DAM, Lal P, Hillman JL, Yang J;  
 PI  
 XX WPI; 2000-387796/33.  
 DR  
 XX N-PSDB; AAA27381.  
 XX  
 XX Immunoglobulin superfamily proteins, the agonist and antagonist of the  
 PT protein is useful for preventing and treating disorders associated with  
 PT altered levels of the protein such as cancer, immune system disorders.  
 XX  
 XX Claim 1; Page 77-78; 105pp; English.  
 PS  
 XX The present sequence is the human immunoglobulin superfamily protein  
 XX IGFAM-1. Its gene was isolated from a cDNA library of synovial membrane  
 CC tissue. It is expressed in reproductive, gastrointestinal and  
 CC cardiovascular tissue, where cancer and inflammation are common. The  
 CC gene, protein, its antibodies, agonists and antagonists are suitable for  
 CC diagnosing and treating many diseases, including cancer, immune system  
 CC disorders (such as inflammation, AIDS, allergies, anaemia,  
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's  
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,  
 CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,  
 CC systemic lupus erythematosus and ulcerative colitis), complications of  
 CC cancer, haemodialysis and extracorporeal circulation, trauma and  
 CC haematopoietic cancer (such as leukaemia) and infections caused by  
 CC bacteria, viruses, fungi or parasites  
 XX  
 XX Sequence 237 AA;  
 SQ

Query Match 91.1%; Score 515.5; DB 3; Length 237;  
 Best Local Similarity 92.7%; Pred. No. 6.6e-29;  
 Matches 101; Conservative 4; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQISINLYNWYQOKPGKAPKLLIYGASSLSQSGVPS 60  
 DB 23 DIQMTQSPSSLSASVGRVTITCRAGQSSISSYLNWYQOKPGKAPKLLIYAASLSQSGVPS 82  
 QY 61 RFGSGSGTDFTLTISSLPEDPATYTCRQSYSTPPECSPFGQGTKEIK 109  
 DB 83 RFGSGSGTDFTLTISSLPEDPATYTCQSYSTPP-ITFGQGTREIK 130  
 RESULT 13  
 ADP22402 ID ADP22402 standard; protein; 107 AA.  
 XX  
 AC ADP22402;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human anti-TNFA antibody light chain variable region SEQ ID NO:308.  
 XX  
 KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostatic cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2004050683-A2.  
 XX  
 XX 17-JUN-2004.  
 XX  
 XX 02-DEC-2003; 2003WO-US038281.  
 PF  
 XX 02-DEC-2002; 2002US-0430729P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 XX  
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulench K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX WPI; 2004-480601/45.  
 DR  
 XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 XX Example 10; SEQ ID NO 308; 213pp; English.  
 PS  
 XX The present invention describes a human monoclonal antibody (1) that  
 XX specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFA in a patient sample, comprising contacting with  
 CC (1), and detecting the level of binding between the antibody and TNFA in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an



CC (Mab) light chain variable region, useful in medicine, pharmacology and  
CC biochemistry. The isotype of a Mab secreted by the human/human hybridoma  
CC Ht was determined to be mu and kappa. Human Mab was purified, and the  
CC antigen recognised by human Mab CLN"-Igm identified by western blotting  
XX  
SQ Sequence 132 AA;

Query Match 90.5%; Score 512; DB 2; Length 132;  
Best Local Similarity 92.7%; Pred. No. 6.9e-29;  
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;  
QY 1 DIQMTQSPSSLSASVGRVTITCRASQISNLYLNWYQKPGKAPKLLIYCASSLQSGVPS 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
23 DIQMTQSPSSLSASVGRVTITCRASQISNLYLNWYQKPGKAPKLLIYAASLQSGVPS 82  
QY 61 RFSGSGGTDFTLTISSLQPEDFATYYCROSYSTPECSFGQGTKLEIK 109  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
83 RFSGSGGTDFTLTISSLQPEDFATYYCQGSYSTPQ--TFGQGTKVEIK 129

Search completed: November 16, 2005, 21:51:37  
Job time : 63.5147 secs

CHARTERED BY THE GOVERNMENT



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 13.0239 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-10  
Perfect score: 566  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QSYSTPPECSTFGQGTKLEIK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	511	90.3	123	2 S40331	Ig kappa chain - h
2	509	89.9	127	2 S40367	Ig kappa chain V-J
3	505	89.2	108	2 B49047	Ig kappa chain V r
4	502	88.7	120	2 S46370	Ig kappa chain V-J
5	500	88.3	129	2 S40317	Ig kappa chain - h
6	491	86.7	129	1 K1HUWK	Ig kappa chain pre
7	489	86.4	108	2 S41122	Ig kappa chain V r
8	489	86.4	108	2 S47182	Ig kappa chain - h
9	485	85.7	108	1 K1HUHU	Ig kappa chain V-I
10	484	85.5	109	2 S31981	Ig kappa chain - h
11	482	85.2	109	2 S31998	Ig kappa chain - h
12	482	85.2	122	2 S40314	Ig kappa chain - h
13	480.5	84.9	107	2 S36275	Ig kappa chain V r
14	476	84.1	129	2 S2793	Ig kappa chain V r
15	475	83.9	117	2 S24206	Ig kappa chain V r
16	474	83.7	108	2 S19674	Ig kappa chain V r
17	473	83.6	122	2 S40370	Ig kappa chain - h
18	472.5	83.5	125	2 S40315	Ig kappa chain - h
19	468	82.7	116	2 A27594	Ig kappa chain pre
20	467	82.5	129	2 S52792	Ig kappa chain V r
21	466	82.3	107	2 S36264	Ig kappa chain V r
22	466	82.3	107	2 S36269	Ig kappa chain V
23	466	82.3	109	2 S31979	Ig kappa chain - h
24	465	82.2	108	2 S31977	Ig kappa chain - h
25	465	82.2	110	2 S44118	Ig kappa chain V-J
26	464.5	82.1	106	2 PC2397	anti-tetanus toxin
27	462	81.6	109	2 S31980	Ig kappa chain - h
28	462	81.6	109	2 S31978	Ig kappa chain - h
29	462	81.6	117	2 S46371	Ig kappa chain V-J

ALIGNMENTS

RESULT 1

S40331  
Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40331  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40331  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-123 <KLE>  
A;Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 511; DB 2; Length 123;  
Best Local Similarity 92.7%; Pred. No. 11e-35;  
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYGASSLQSGVPS 60  
Db 17 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKAPKLLIYGASSLQSGVPS 76  
Qy 61 RFGSGSGTDTLTITISLQPEDFATYCYCROSYSYTPPECSTFGQGTKLEIK 109  
Db 77 RFGSGSGTDTLTITISLQPEDFATYCYCROSYSYTPPECSTFGQGTKLEIK 123

RESULT 2

S40367  
Ig kappa chain V-J-C region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40367  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40367  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-127 <KLE>  
A;Cross-references: EMBL:X72477  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 89.9%; Score 509; DB 2; Length 127;

```

Best Local Similarity 91.7%; Pred. No. 1.6e-35;
Matches 100; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 18 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYAASSLSQSGVPS 77

Qy 61 RFSGSGSGTDFTLTISLQPEDFATYYCQSYSTPPECSEFGQGTKEIK 109
Db 78 RFSGSGSGTDFTLTISLQPEDFATYYCQSYSTP--WTFGGTKVEIK 124

RESULT 3
Bg49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: B49047
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A:Experimental source: thymic B lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIPI:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 505; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 2.9e-35;
Matches 100; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISLQPEDFATYYCQSYSTPPECSEFGQGTKEIK 109
Db 61 RFSGSGSGTDFTLTISLQPEDFATYYCQSYSTP--LTFGGTKVEIK 107

RESULT 4
S46370
Ig kappa chain V-J region (T23-9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46370; S38644
R:Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46370
A:Molecule type: mRNA
A:Residues: 1-120 <BEN>
A:Cross-references: EMBL:227171; NID:9415957; PIDN:CAA81695.1; PID:9415958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 88.7%; Score 502; DB 2; Length 120;
Best Local Similarity 88.9%; Pred. No. 5.7e-35;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 11 DIQMTQSPSSLSASVGDRTVITCRASRISISFLNWKYQKPKAPOLLIVAVSRSLQSGVPS 70

Qy 61 RFSGSGSGTDFTLTISLQPEDFATYYCQSYSTPPECSEFGQGTKEIK 108

```

```

Db 71 RFSGSGSGTDFTLTISLQPEDFATYYCQSFNSNPPEVTFQGTKEIK 118

RESULT 5
S40317
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40317
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:9408091; PMID:8258341
A:Accession: S40317
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: EMBL:X72427; NID:9441322; PIDN:CAA51095.1; PID:9441323
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 500; DB 2; Length 129;
Best Local Similarity 89.0%; Pred. No. 9e-35;
Matches 97; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 22 DIQMTQSPSSLSLSDRVTITCRASQISGYLNWYQKPKAPKLLIYGASSLSQSGVPS 81

Qy 61 RFSGSGSGTDFTLTISLQPEDFATYYCQSYSTPPECSEFGQGTKEIK 109
Db 82 RFSGSGSGTDFTLTISLQPEDFATYYCQSYSTPP--TFGGTKVEIK 128

RESULT 6
K1HUWK
Ig kappa chain precursor V-I region (Walker) - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
R:Klobeck, H.G.; Combratio, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A:Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines
A:Reference number: A93534; MUID:85014148; PMID:6091049
A:Accession: A01883
A:Molecule type: DNA
A:Residues: 1-129 <KLO>
A:Cross-references: UNIPROT:P04431
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two heavy (lambda) chains. In some cases, such as IGA and IGM, the subunits associate into a dimer.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-123/Product: Ig kappa chain V-I region (Walker) #status predicted <MAT>
F:23-45/Region: framework 1
F:38-112/Domain: immunoglobulin homology <IMM>
F:46-56/Region: complementarity-determining 1
F:57-71/Region: framework 2
F:72-78/Region: complementarity-determining 2
F:79-110/Region: framework 3
F:111-119/Region: complementarity-determining 3
F:120-129/Region: framework 4
F:45-110/Disulfide bonds: #status predicted

Query Match 86.7%; Score 491; DB 1; Length 129;
Best Local Similarity 90.8%; Pred. No. 5e-34;
Matches 99; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

```

```
Qy 1 DIQMTQSPSSLSASVGRVITTCRASQISINLYNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 23 DIQMTQSPSSLSASVGRVITTCRASQISINLYNWYQKPKAPKLLIYAASSLSQSGVTS 82
Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSSYSTPPPCSFQGGTKLEIK 109
Db 83 RFSGSGSGTDFTLTISSLQPEDSATYYCQOSYST--LITFGQGRLEIK 129

RESULT 7
S44122
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44122
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Status: preliminary
A;Accession: S44122
A;Molecule type: DNA
A;Residues: 1-108 <HAW>
A;Cross-references: EMBL:Z31390; NID:9472976; PIDN:CAA83265.1; PID:9940533
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 489; DB 2; Length 108;
Best Local Similarity 89.9%; Pred. No. 6.2e-34; Mismatches 5; Indels 2; Gaps 1;
Matches 98; Conservative 4;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQISINLYNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQISINLYNWYQKLGKAPKLLIYGASSLSQSGVPS 60
Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSSYSTPPPCSFQGGTKLEIK 109
Db 61 TFSGSGSGTDFTLTISSLQPEDFAIYYCQOSYSTP--WTFGQGRKVEIK 107

RESULT 8
S47182
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47182
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IGM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
A;Accession: S47182
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MC1>
A;Cross-references: EMBL:X79786; NID:9506422; PIDN:CAA56182.1; PID:9506423
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 489; DB 2; Length 108;
Best Local Similarity 88.1%; Pred. No. 6.2e-34; Mismatches 7; Indels 2; Gaps 1;
Matches 96; Conservative 7;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQISINLYNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 1 ETELTQSPSSLSASVGRVITTCRASQISINLYNWYQKPKAPKLLIYAASSLSQSGVPS 60
Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSSYSTPPPCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQOSYSTP--ITSGQGRLEIK 107
```

```
RESULT 9
K1HUHU
Ig kappa chain V-I region (Hau) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A01868; S02574
R;Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970
A;Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg;
A;Reference number: A01868; MUID:71032830; PMID:4097974
A;Accession: A01868
A;Molecule type: protein
A;Residues: 1-108 <WAT>
A;Cross-references: UNIPROT:P01600
A;Note: the C region of this chain has the Inv (3) marker
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the;
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into la;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 85.7%; Score 485; DB 1; Length 108;
Best Local Similarity 87.2%; Pred. No. 1.3e-33; Mismatches 4; Indels 2; Gaps 1;
Matches 95; Conservative 8;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQISINLYNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQISINLYNWYQKPKAPQVLLIYAASSLSQSGVPS 60
Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSSYSTPPPCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITP--TSPGQGRVEIK 107

RESULT 10
S31981
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31981
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31981
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: EMBL:Z15077; NID:938493; PIDN:CAA78786.1; PID:938494
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 484; DB 2; Length 109;
Best Local Similarity 86.2%; Pred. No. 1.6e-33; Mismatches 8; Indels 2; Gaps 1;
Matches 94; Conservative 8;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQISINLYNWYQKPKAPKLLIYGASSLSQSGVPS 60
Db 1 ELVMTQSPSSLSASVGRVITTCRASQDISRYLNWYQKPKAPKLLIHGASTLESQSGVP 60
```

Qy 61 RFSGSGGTDFTLTITSSIQPEDFATYYCRQSYSTPECSFGQGTKEIK 109  
|||||  
Db 61 RFSGSGGTDFTLTITSSIQPEDFATYYCQSYSTP--FTFGGTKEIK 107  
|||||  
RESULT 11  
S31998  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S31998  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S31998  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
A:Cross-references: EMBL:Z15081; NID:g38501; PIDN:CAA78790.1; PID:g38502  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
Query Match 85.2%; Score 482; DB 2; Length 109;  
Best Local Similarity 87.2%; Pred. No. 2.4e-33;  
Matches 95; Conservative 6; Mismatches 6; Indels 2; Gaps 1;  
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60  
:: |||||  
Db 1 ELVMTQSPSSLSASVGDRTVITCRASQISAYLNWYQKPKAPKLLIYSASSLSQSGVPS 60  
|||||  
Qy 61 RFSGSGGTDFTLTITSSIQPEDFATYYCRQSYSTPECSFGQGTKEIK 109  
|||||  
Db 61 RFSGSGGTDFTLTITSSIQPEDFATYYCQSYSTP--WTFGHGTVKEIK 107  
|||||  
RESULT 12  
S40314  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40314  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40314  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-122 <KLE>  
A:Cross-references: EMBL:X72424  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-105/Domain: immunoglobulin homology <IMM>  
Query Match 85.2%; Score 482; DB 2; Length 122;  
Best Local Similarity 86.2%; Pred. No. 2.6e-33;  
Matches 94; Conservative 7; Mismatches 6; Indels 2; Gaps 1;  
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60  
|||  
Db 16 DIQMTQSPSSLSASVGDRTVITCRASQISNNYLNWYQKPKAPNLLISAASSLSQSGVPS 75  
|||||  
Qy 61 RFSGSGGTDFTLTITSSIQPEDFATYYCRQSYSTPECSFGQGTKEIK 109  
|||||  
Db 76 RFSGSGGTDFTLTITSSIQPEDFGTYCQQTHTTTP--TFGGGTKEIK 122  
|||||  
RESULT 13  
S36275  
Ig lambda chain V region (clone alpha-FOG1-A4) - human (fragment)  
C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: S36275  
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36275  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-107 <GRI>  
A:Cross-references: EMBL:Z18827; NID:g33416; PIDN:CAA79279.1; PID:g939909  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
Query Match 84.9%; Score 480.5; DB 2; Length 107;  
Best Local Similarity 87.2%; Pred. No. 3.1e-33;  
Matches 95; Conservative 4; Mismatches 7; Indels 3; Gaps 1;  
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60  
|||  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLAWYQKPKGVPKLLIYAASTLSQSGVPS 60  
|||||  
Qy 61 RFSGSGGTDFTLTITSSIQPEDFATYYCRQSYSTPECSFGQGTKEIK 109  
|||||  
Db 61 RFSGSGGTDFTLTITSSIQPEDVAVYCCQYISTP---TFGGGTKEIK 106  
|||||  
RESULT 14  
S52793  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
C:Accession: S52793  
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,  
submitted to the EMBL Data Library, March 1995  
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma  
A:Reference number: S52789  
A:Accession: S52793  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <ROC>  
A:Cross-references: EMBL:X85997; NID:g758600; PIDN:CAA59989.1; PID:g758601  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-112/Domain: immunoglobulin homology <IMM>  
Query Match 84.1%; Score 476; DB 2; Length 129;  
Best Local Similarity 85.3%; Pred. No. 8.8e-33;  
Matches 93; Conservative 8; Mismatches 6; Indels 2; Gaps 1;  
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60  
|||||  
Db 23 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKAPKLLIYAAASSLSQSGVPA 82  
|||||  
Qy 61 RFSGSGGTDFTLTITSSIQPEDFATYYCRQSYSTPECSFGQGTKEIK 109  
|||||  
Db 83 RFVSGSGGTDFTLTITSSIQPEDFATYYCQYISAP--LTFGGGTKEIK 129  
|||||  
RESULT 15  
S24206  
Ig kappa chain V region (Vx O12 and Vx O2) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 25-Feb-1994 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C:Accession: S24206; S24209  
R:Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.  
Eur. J. Immunol. 21, 1821-1827, 1991  
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated O regi  
A:Reference number: S24205; MUID:91330953; PMID:1907917  
A:Accession: S24206  
A:Molecule type: DNA  
A:Residues: 1-117 <PAR>



RECEIVED

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 61.1121 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-10

Perfect score: 566

Sequence: 1 DIQWTSPLSASVGDVRT.....QSYSTPPCSFGQGTKEIK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:\*

1: uniprot\_sprot;\*

2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	497.5	87.9	107	2 Q96SA9	Q96SA9 homo sapien
2	496	87.6	108	2 Q9UL77	Q9UL77 homo sapien
3	491	86.7	129	1 KV1W HUMAN	P04431 homo sapien
4	485	85.7	108	1 KV1H HUMAN	P01600 homo sapien
5	475.5	84.0	107	2 Q9UL81	Q9UL81 homo sapien
6	473	83.6	236	2 Q6GMW1	Q6GMW1 homo sapien
7	471	83.2	236	2 Q6GMX0	Q6GMX0 homo sapien
8	467	82.5	236	2 Q6GMX8	Q6GMX8 homo sapien
9	465	82.2	236	2 Q7Z3Y4	Q7Z3Y4 homo sapien
10	461	81.4	108	1 KV1N HUMAN	P01606 homo sapien
11	461	81.4	236	2 Q6PIH7	Q6PIH7 homo sapien
12	460	81.3	108	2 Q9UL70	Q9UL70 homo sapien
13	459	81.1	108	1 KV1E HUMAN	P01597 homo sapien
14	450	79.5	108	1 KV1M HUMAN	P01605 homo sapien
15	449.5	79.4	109	1 KV1T HUMAN	P01612 homo sapien
16	449	79.3	108	1 KV1R HUMAN	P01610 homo sapien
17	449	79.3	108	2 Q9UL79	Q9UL79 homo sapien
18	448	79.2	108	1 KV1G HUMAN	P01599 homo sapien
19	446	78.8	108	1 KV1Y HUMAN	P80362 homo sapien
20	444	78.4	108	1 KV1O HUMAN	P01607 homo sapien
21	442	78.1	108	1 KV1B HUMAN	P01594 homo sapien
22	442	78.1	108	1 KV1V HUMAN	P04430 homo sapien
23	441	77.9	108	1 KV1S HUMAN	P01611 homo sapien
24	440	77.7	108	1 KV1F HUMAN	P01598 homo sapien
25	437	77.2	108	1 KV1A HUMAN	P01593 homo sapien
26	437	77.2	244	2 Q65ZC8	Q65ZC8 homo sapien
27	435	76.9	234	2 Q7Z473	Q7Z473 homo sapien
28	435	76.9	236	2 Q6PIH4	Q6PIH4 homo sapien
29	434	76.7	108	1 KV1K HUMAN	P01603 homo sapien
30	434	76.7	236	2 Q6GMX9	Q6GMX9 homo sapien
31	433	76.5	108	1 KV1P HUMAN	P01608 homo sapien

32	432	76.3	240	2 Q65ZC9	Q65ZC9 homo sapien
33	431.5	76.2	107	1 KV1D HUMAN	P01596 homo sapien
34	430	76.0	108	1 KV1Q HUMAN	P01609 homo sapien
35	427	75.4	108	1 KV1C HUMAN	P01595 homo sapien
36	427	75.4	129	1 KV1X HUMAN	P04432 homo sapien
37	427	75.4	236	2 Q6PI75	Q6PI75 homo sapien
38	425	75.1	108	1 KV1L HUMAN	P01604 homo sapien
39	425	75.1	117	1 KV1J HUMAN	P01602 homo sapien
40	417	73.7	117	1 KV1I HUMAN	P01601 homo sapien
41	407	71.9	116	2 Q96PF6	Q96PF6 homo sapien
42	403	71.2	108	1 KV5M MOUSE	P01646 mus musculu
43	403	71.2	114	1 KV4A HUMAN	P01625 homo sapien
44	399	70.5	108	1 KV5J MOUSE	P01643 mus musculu
45	397	70.1	109	2 Q920E6	Q920E6 mus musculu

#### ALIGNMENTS

RESULT 1  
Q96SA9 ID Q96SA9 PRELIMINARY; PRT; 107 AA.  
AC Q96SA9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain  
DE variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98375893; PubMed=9712075;  
RA Aderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin  
RT antibody V region genes";  
RL J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96396; AAB68785.1; -;  
DR PIR; B49047; B49047;  
DR PIR; PH0867; PH0867;  
DR PIR; S16840; S16840.  
DR PIR; S31977; S31977.  
DR PIR; S34083; S34083.  
DR PIR; S34086; S34086.  
DR HSSP; P01607; IBMW  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 87.9%; Score 497.5; DB 2; Length 107;  
Best Local Similarity 90.8%; Pred. No. 8.2e-42;  
Matches 99; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy	1	DIQWTSPLSASVGDVRTITCRASQISNYLNWYQKPKAPKLLIYGASSLSQGVPS	60
Db	1	DIQWTSPLSASVGDVRTITCRASQISNYLNWYQKPKAPKLLIYAASSLSQGVPS	60
Qy	61	RFGSGSGTFTLTISLQPEDFATYTCROSYSPPPCSFQGTKEIK	109
Db	61	RFGSGSGTFTLTISLQPEDFATYTCROSYSPPPCSFQGTKEIK	106

RESULT 2  
Q9UL77 ID Q9UL77 PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;

```
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=38277139; PubMed=3614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 87.6%; Score 496; DB 2; Length 108;
Best Local Similarity 89.9%; Pred. No. 1.2e-41;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Oy 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60
Oy 61 RFSGSGSGDTFTLTISLQPEDFATYYCROSYSTPPESFGQGTKEIK 109
Db 61 RFSGSGSGDTFTLTISLQPEDFATYYCROSYST--SWTFEGGTKEIK 107

RESULT 3
KV1W HUMAN
ID_KV1W HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUW.
DR HSSP; P01607; 1BWW.
```

```
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 22
FT CHAIN 23
FT DOMAIN 23
FT DOMAIN 46
FT DOMAIN 57
FT DOMAIN 71
FT DOMAIN 72
FT DOMAIN 78
FT DOMAIN 79
FT DOMAIN 111
FT DOMAIN 119
FT DOMAIN 120
FT DISULFID 45
FT NON_TER 129
FT NON_TER 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 86.7%; Score 491; DB 1; Length 129;
Best Local Similarity 90.8%; Pred. No. 4.5e-41;
Matches 99; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Oy 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60
Db 23 DIQWTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQSGVTS 82
Oy 61 RFSGSGSGDTFTLTISLQPEDFATYYCROSYSTPPESFGQGTKEIK 109
Db 83 RFSGSGSGDTFTLTISLQPEDSATYYCQOSYST--LITFGQGTREIK 129

RESULT 4
KV1H HUMAN
ID_KV1H HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; K1HUH.
DR PDB; 1F6L; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1
FT DOMAIN 23
FT DOMAIN 24
FT DOMAIN 35
FT DOMAIN 49
FT DOMAIN 50
FT DOMAIN 56
```



```
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match
Best Local Similarity 85.7%; Score 485; DB 1; Length 108;
Matches 95; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
Db 1 DIQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPQVLLIYAASSLSQGVPS 60
Qy 61 RFSGSGSGTDFTLTISLQPEDFATYICROSYSPTPPSCSFGQGTKEIK 109
Db 61 RFSGSGSGTDFTLTISLQPEDFATYICQNYITP--TSFGQGTKEIK 107

RESULT 5
Q9UL81 PRELIMINARY; PRT; 107 AA..
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 107 107
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match
Best Local Similarity 84.08%; Score 475.5; DB 2; Length 107;
Matches 94; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

Qy 1 DIQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60
Db 1 DIQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPNLLIYAASSLSQGVPS 60
Qy 61 RFSGSGSGTDFTLTISLQPEDFATYICROSYSPTPPSCSFGQGTKEIK 109
Db 61 RFSGSGSGTDFTLTISLQPEDFATYICQSYSA--LTFPGTKVDIR 106

RESULT 6
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Splettenstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00407; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein_MHC;
SQ SEQUENCE 236 AA; 25751 MW; 5BF6A087AFAC437 CRC64;

Query Match
Best Local Similarity 83.6%; Score 473; DB 2; Length 236;
Matches 95; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

Qy 2 IQWQSPSSLSASVGRVITTCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPSR 61
Db 24 IQWQSPSSLSASVGRVITTCRASQISNDLGMWYQKPGKAPKLLIYAASSLSQGVPSR 83
Qy 62 FSGSGSGTDFTLTISLQPEDFATYICROSYSPTPPSCSFGQGTKEIK 109
Db 84 FSGSGSGTDFTLTISLQPEDFATYICLDYNYP--WTFQGTKEIK 129

RESULT 7
Q6GMX0 PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
```

```

RN  SEQUENCE FROM N.A.
RP  TISSUE=Spleen;
RX  MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Schetz T.E.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Richards S., Wozley K.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP  SEQUENCE FROM N.A.
RC  TISSUE=Spleen;
RA  Strausberg R.;
RL  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC073775; AAH73775.1; -.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig-cl.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF07654; Cl-set; 1.
DR  SMART; SM00409; IG; 2.
DR  SMART; SM00407; IGcl; 1.
DR  SMART; SM00406; IGV; 1.
DR  SMART; SM00407; IGcl; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS00835; IG_LIKE; 2.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW  Hypothetical protein.
SQ  SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 83.2%; Score 471; DB 2; Length 236;
Best Local Similarity 84.4%; Pred. No. 8.9e-39;
Matches 92; Conservative 8; Mismatches 7; Indels 2; Gaps 1;

Qy 1 DIQWTSPLSASVGDRTVITCRASQISNLYNWYQKPKAPKLLIYGASSLSQGVPS 60
Db 23 DIQWTSPLSASVGDRTVITCRASQINLYNWYQLKPKAPNLLIYAASSLSQGVPS 82

Qy 61 RFSGSGSGTDTLTITSIQLPEDPATYCYCROSYSTPPECDFGQGTKEIK 109
Db 83 RFSGSGSGTDTLTITSIQLRPDPATYCYCQSYNIP--LTFGGGINVEIK 129

RESULT 8
Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Schetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Wozley K.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 83.2%; Score 471; DB 2; Length 236;
Best Local Similarity 84.4%; Pred. No. 8.9e-39;
Matches 92; Conservative 8; Mismatches 7; Indels 2; Gaps 1;

Qy 1 DIQWTSPLSASVGDRTVITCRASQISNLYNWYQKPKAPKLLIYGASSLSQGVPS 60
Db 23 DIQWTSPLSASVGDRTVITCRASQINLYNWYQLKPKAPNLLIYAASSLSQGVPS 82

Qy 61 RFSGSGSGTDTLTITSIQLPEDPATYCYCROSYSTPPECDFGQGTKEIK 109
Db 83 RFSGSGSGTDTLTITSIQLRPDPATYCYCQSYNIP--LTFGGGINVEIK 129

RESULT 8
Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Schetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Wozley K.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 82.5%; Score 467; DB 2; Length 236;
Best Local Similarity 84.4%; Pred. No. 2.2e-38;
Matches 92; Conservative 9; Mismatches 6; Indels 2; Gaps 1;

Qy 1 DIQWTSPLSASVGDRTVITCRASQISNLYNWYQKPKAPKLLIYGASSLSQGVPS 60
Db 23 DIQWTSPLSASVGDRTVITCRASQISNLYNWYQKPKAPKLLIYAASSLSQGVPS 82

Qy 61 RFSGSGSGTDTLTITSIQLPEDPATYCYCROSYSTPPECDFGQGTKEIK 109
Db 83 RFSGSGSGTDTLTITSIQLPEDPATYCYCQAHSPF--FTFGGTVKDIK 129

RESULT 9
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```



RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

```
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
```

Query Match 81.4%; Score 461; DB 2; Length 236;  
Best Local Similarity 83.5%; Pred. No. 8.8e-38;  
Matches 91; Conservative 8; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLWYQKPKAPKLLIYGASSLSQGVPS 60

Db 23 DIQMTQSPSSLSASVGDRTVITCRASQISNYLWYQKPKAPKLLIYGASSLSQGVPS 82

Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYTCROSYSSTPPECSEFGQTKLEIK 109

Db 83 RFSGSGSGTEFTLTISSLQPEDFATYTCQQLNSGPP--TFGGGTKVEIK 129

RESULT 12

```
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe F.L., Kalis N.N., Berney S.N.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig.v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
```

Query Match 81.3%; Score 460; DB 2; Length 108;  
Best Local Similarity 85.3%; Pred. No. 4.5e-38;  
Matches 93; Conservative 4; Mismatches 10; Indels 2; Gaps 2;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLWYQKPKAPKLLIYGASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLWYQKPKAPKLLIYGASSLSQGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYTCROSYSSTPPECSEFGQTKLEIK 109

Db 61 RFSGSGSGTDFTLTISSLQPEDFATYTCQYNSAPR--TFGGGTKVEIK 107

RESULT 13

```
KVIE_HUMAN
ID KVIE_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-1 region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P.; Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
DR PIR; A01865; K1HUDE.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
DR PROSITE; PS50835; IG LIKE; 1.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;
```

Query Match 81.1%; Score 459; DB 1; Length 108;  
Best Local Similarity 80.6%; Pred. No. 5.6e-38;  
Matches 87; Conservative 12; Mismatches 7; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLWYQKPKAPKLLIYGASSLSQGVPS 60

Db 1 BIZMTQSPSSLSASVGDRTVITCRAGQSVNKYLNWYQKPKAPKLLIYFAASSLSKGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYTCROSYSSTPPECSEFGQTKLEI 108

Db 61 RFSGSGSGTDFTLTISGLLPEDFATYTCQOSYVTP--YTFGPGTKVEM 106

RESULT 14

```
KVIM_HUMAN
ID KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-1 region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IgM
```



CONFIDENTIAL

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.534 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357a-10

Perfect score: 566

Sequence: 1 DIQMTSPSPSLASVGDVRT.....QSYTPPECSFGQGTKLEIK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	511	90.3	240	4	US-09-192-854-2
2	505.5	89.3	108	3	US-09-240-274-32
3	505.5	89.3	108	3	US-09-240-274-43
4	505	89.2	108	2	US-08-379-057-29
5	504	89.0	108	3	US-09-025-769B-14
6	504	89.0	108	4	US-09-490-070A-14
7	504	89.0	108	4	US-09-490-153-14
8	504	89.0	108	4	US-09-490-324-14
9	501.5	88.6	108	3	US-09-240-274-167
10	500	88.3	109	3	US-09-025-769B-28
11	500	88.3	109	3	US-09-025-769B-43
12	500	88.3	109	4	US-09-490-070A-28
13	500	88.3	109	4	US-09-490-070A-43
14	500	88.3	109	4	US-09-490-153-28
15	500	88.3	109	4	US-09-490-153-43
16	500	88.3	109	4	US-09-490-324-28
17	500	88.3	109	4	US-09-490-324-43
18	499	88.2	107	1	US-08-276-852-105
19	499	88.2	107	1	US-08-899-575-105
20	499	88.2	107	1	US-08-899-575-105
21	499	88.2	107	5	PCT-US95-08743-105
22	498	88.0	107	1	US-08-276-852-104
23	498	88.0	107	1	US-08-899-575-104
24	498	88.0	107	1	US-08-899-575-104
25	498	88.0	107	5	PCT-US95-08743-104
26	497	87.8	107	3	US-09-240-274-158
27	496.5	87.7	108	1	US-08-276-852-109

28 496.5 87.7 108 1 US-08-899-575-109 Sequence 109, App  
29 496.5 87.7 108 1 US-08-899-575-109 Sequence 109, App  
30 496.5 87.7 108 5 PCT-US95-08743-109 Sequence 109, App  
31 496 87.6 107 3 US-09-240-274-37 Sequence 37, Appl  
32 495.5 87.5 108 3 US-09-240-274-41 Sequence 41, Appl  
33 494 87.3 107 3 US-09-240-274-156 Sequence 156, App  
34 494 87.3 107 3 US-09-240-274-175 Sequence 175, App  
35 494 87.3 107 3 US-09-240-274-176 Sequence 176, App  
36 492 86.9 107 3 US-09-240-274-168 Sequence 168, App  
37 492 86.9 107 3 US-09-240-274-168 Sequence 168, App  
38 491.5 86.8 108 3 US-09-240-274-181 Sequence 181, App  
39 491.5 86.8 114 2 US-08-561-521-43 Sequence 43, Appl  
40 491.5 86.8 114 5 PCT-US95-01219-43 Sequence 43, Appl  
41 491 86.7 107 2 US-08-552-558-36 Sequence 36, Appl  
42 491 86.7 107 2 US-08-378-939-14 Sequence 14, Appl  
43 491 86.7 214 4 US-09-472-087-71 Sequence 71, Appl  
44 488 86.2 107 3 US-09-240-274-38 Sequence 38, Appl  
45 488 86.2 107 3 US-09-240-274-39 Sequence 39, Appl

#### ALIGNMENTS

RESULT 1

US-09-192-854-2

; Sequence 2, Application US/09192854

; Patent No. 6696245

; GENERAL INFORMATION:

; APPLICANT: Winter, Greg

; APPLICANT: Tomlinson, Ian

; TITLE OF INVENTION: Methods for Selecting Functional Peptides

; FILE REFERENCE: 3789/72916

; CURRENT APPLICATION NUMBER: US/09/192,854

; CURRENT FILING DATE: 1998-11-17

; EARLIER APPLICATION NUMBER: 60/066,729

; EARLIER FILING DATE: 1997-11-21

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 2

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-192-854-2

Query Match 90.3%; Score 511; DB 4; Length 240;  
Best Local Similarity 92.7%; Pred. No. 2.4e-39;  
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;  
Qy 1 DIQMTSPSPSLASVGDVRTITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 60  
Db 133 DIQMTSPSPSLASVGDVRTITCRASQISNYLNWYQKPKAPKLLIYGASSLSQSGVPS 192  
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYVCROSYSTPPECSFGQGTKLEIK 109  
Db 193 RFGSGSGTDTLTITSSLOPEDFATYVCROSYSTPN--TFGQGTKVEIK 239

RESULT 2

US-09-240-274-32

; Sequence 32, Application US/09240274

; Patent No. 6255455

; GENERAL INFORMATION:

; APPLICANT: Siegel, Donald L.

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

; FILE REFERENCE: 09596-4202

; CURRENT APPLICATION NUMBER: US/09/240,274

; CURRENT FILING DATE: 1999-01-29

; EARLIER APPLICATION NUMBER: 60/081,380

; EARLIER FILING DATE: 1998-04-10

; EARLIER APPLICATION NUMBER: 60/028,550

; NUMBER OF SEQ ID NOS: 224

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-32

Query Match      89.3%; Score 505.5; DB 3; Length 108;
Best Local Similarity 92.5%; Pred. No. 3.2e-39;
Matches 99; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy  3 QMTQSPSSLSASVGRVTITCRASQISINYLNWYQKPGKAPKLLIYGASSLQSGVPSRF 62
Db  2 ELTQSPSSLSASVGRVTITCRASQISINYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61

Qy  63 SGSGSGTDTLTITSLQPEDFATYVCROSSTPPPCSFQGTGLEIK 109
Db  62 SGSGSGTDTLTITSLQPEDFATYVCQSYSTPP-YTFGQGTGLEIK 107

RESULT 3
US-09-240-274-43
; Sequence 43, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-43

Query Match      89.3%; Score 505.5; DB 3; Length 108;
Best Local Similarity 92.5%; Pred. No. 3.2e-39;
Matches 99; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy  3 QMTQSPSSLSASVGRVTITCRASQISINYLNWYQKPGKAPKLLIYGASSLQSGVPSRF 62
Db  2 ELTQSPSSLSASVGRVTITCRASQISINYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61

Qy  63 SGSGSGTDTLTITSLQPEDFATYVCROSSTPPPCSFQGTGLEIK 109
Db  62 SGSGSGTDTLTITSLQPEDFATYVCQSYSTPP-YTFGQGTGLEIK 107

RESULT 4
US-08-379-057-29
; Sequence 29, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jorgen
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; OTHER INFORMATION: Different Epitopes of Human gp39 and Methods For Their Use
```

```
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,057
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0133-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-379-057-29

Query Match      89.2%; Score 505; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 3.6e-39;
Matches 100; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy  1 DIQMTQSPSSLSASVGRVTITCRASQISINYLNWYQKPGKAPKLLIYGASSLQSGVPS 60
Db  1 DIQMTQSPSSLSASVGRVTITCRASQISINYLNWYQKPGKAPKLLIYAASSLQSGVPS 60

Qy  61 RFSGSGSGTDTLTITSLQPEDFATYVCROSSTPPPCSFQGTGLEIK 109
Db  61 RFSGSGSGTDTLTITSLQPEDFATYVCQSYSTPP--LTFGGGTKVEIK 107

RESULT 5
US-09-025-769B-14
; Sequence 14, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
```



```
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-14

Query Match      89.0%; Score 504; DB 3; Length 108;
Best Local Similarity 91.7%; Pred. No. 4.4e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQQKPGKAPKLLIYGASSLSQGVPS 60
   |||||
DB 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQQKPGKAPKLLIYAASSLSQGVPS 60
   |||||
QY 61 RFGSGSGTDFLTITSSLOPEDPATYVCROSYSTPECSFGQGTKEIK 109
   |||||
DB 61 RFGSGSGTDFLTITSSLOPEDPATYVCQYYSTP--LTFGGGTKVEIK 107

RESULT 6
US-09-490-070A-14
; Sequence 14, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
```

```
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-070A-14

Query Match      89.0%; Score 504; DB 4; Length 108;
Best Local Similarity 91.7%; Pred. No. 4.4e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQQKPGKAPKLLIYGASSLSQGVPS 60
   |||||
DB 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQQKPGKAPKLLIYAASSLSQGVPS 60
   |||||
QY 61 RFGSGSGTDFLTITSSLOPEDPATYVCROSYSTPECSFGQGTKEIK 109
   |||||
DB 61 RFGSGSGTDFLTITSSLOPEDPATYVCQYYSTP--LTFGGGTKVEIK 107

RESULT 7
US-09-490-153-14
; Sequence 14, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-153-14
```

Query Match 89.0%; Score 504; DB 4; Length 108;  
Best Local Similarity 91.7%; Pred. No. 4.4e-39;  
Matches 100; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTSPSSLSASVGDVRTITCRASQISINLYNWYQKPGKAPKLLIYGASSLSQSGVPS 60  
Db 1 DIQMTSPSSLSASVGDVRTITCRASQISINLYNWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPQDFATYYCQSYSTPPECDFGQGTKEIK 109  
Db 61 RFGSGSGTDFTLTISSLPQDFATYYCQSYSTP--LTFGGGKVEIK 107

RESULT 8  
US-09-490-324-14  
; Sequence 14, Application US/09490324  
; Patent No. 6828422  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,324  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-490-324-14

Query Match 89.0%; Score 504; DB 4; Length 108;  
Best Local Similarity 91.7%; Pred. No. 4.4e-39;  
Matches 100; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTSPSSLSASVGDVRTITCRASQISINLYNWYQKPGKAPKLLIYGASSLSQSGVPS 60  
Db 1 DIQMTSPSSLSASVGDVRTITCRASQISINLYNWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPQDFATYYCQSYSTPPECDFGQGTKEIK 109  
Db 61 RFGSGSGTDFTLTISSLPQDFATYYCQSYSTP--LTFGGGKVEIK 107

Db 61 RFGSGSGTDFTLTISSLPQDFATYYCQYYSTP--LTFGGGKVEIK 107

RESULT 9  
US-09-240-274-167  
; Sequence 167, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 167  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH34  
US-09-240-274-167

Query Match 88.6%; Score 501.5; DB 3; Length 108;  
Best Local Similarity 91.6%; Pred. No. 7.5e-39;  
Matches 98; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Qy 3 QMTQSPSSLSASVGDVRTITCRASQISINLYNWYQKPGKAPKLLIYGASSLSQSGVPSRF 62  
Db 2 ELTQSPSSLSASVGDVRTITCRASQISINLYNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61

Qy 63 SGSGSGTDFTLTISSLPQDFATYYCQSYSTPPECDFGQGTKEIK 109  
Db 62 SGSGSGTDFTLTISSLPQDFATYYCQSYSTP--YTFGGGKLEIK 107

RESULT 10  
US-09-025-769B-28  
; Sequence 28, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:

```
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-28

Query Match      88.3%; Score 500; DB 3; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKGKAPKLLIYGASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKGKAPKLLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPESFGQGTKEIK 109
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCQOHTTTP--TFGQGTKEIK 107

RESULT 11
US-09-025-769B-43
; Sequence 43, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-43
```

```
Query Match      88.3%; Score 500; DB 3; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKGKAPKLLIYGASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKGKAPKLLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPESFGQGTKEIK 109
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCQOHTTTP--TFGQGTKEIK 107

RESULT 12
US-09-490-070A-28
; Sequence 28, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-490-070A-28

Query Match      88.3%; Score 500; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKGKAPKLLIYGASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISNYLNWYQKPKGKAPKLLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPESFGQGTKEIK 109
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCQOHTTTP--TFGQGTKEIK 107
```

61 RFGSGSGTDTLTITSSLPQEDFATYYCQHYHTTP--TFQGGTKVEIK 107

Db

RESULT 13

US-09-490-070A-43

; Sequence 43, Application US/09490070A

; Patent No. 6696248

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

; White & McAuiffie

; STREET: 1666 K Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,070A

; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Colin G. Sandercock, Esq.

; REGISTRATION NUMBER: 31,298

; REFERENCE/DOCKET NUMBER: 37629-0005

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 912-2000

; TELEFAX: (202) 912-2020

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 109 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-09-490-070A-43

Query Match 88.3%; Score 500; DB 4; Length 109;

Best Local Similarity 89.9%; Pred. No. 1e-38;

Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Oy

1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKGKAPKLLIYGASSLSQSGVPS 60

Db

1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKGKAPKLLIYAASSLSQSGVPS 60

Oy

61 RFGSGSGTDTLTITSSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109

Db

61 RFGSGSGTDTLTITSSLPQEDFATYYCQHYHTTP--TFQGGTKVEIK 107

RESULT 14

US-09-490-153-28

; Sequence 28, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,153

; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 596-9000

; TELEFAX: (212) 596-9090

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 109 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-490-153-28

Query Match 88.3%; Score 500; DB 4; Length 109;

Best Local Similarity 89.9%; Pred. No. 1e-38;

Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Oy

1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKGKAPKLLIYGASSLSQSGVPS 60

Db

1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPKGKAPKLLIYAASSLSQSGVPS 60

Oy

61 RFGSGSGTDTLTITSSLPQEDFATYYCRQSYSTPPSCSFQGGTKLEIK 109

Db

61 RFGSGSGTDTLTITSSLPQEDFATYYCQHYHTTP--TFQGGTKVEIK 107

RESULT 15

US-09-490-153-43

; Sequence 43, Application US/09490153

; Patent No. 6706484

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

```

;
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-490-153-43
```

```

Query Match      88.3%; Score 500; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQOKPKAPKLLIYGASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQOKPKAPKLLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISLSQPEDFATYYCROSYSTPPPCSFQGTKEIK 109
Db 61 RFGSGSGTDFTLTISLSQPEDFATYYCQHHYTPP--TFGQGTKEIK 107
```

Search completed: November 16, 2005, 22:07:18  
Job time : 18.534 secs

10/23/54 10:00 AM 10:00 AM 10:00 AM

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 66.9228 Seconds  
(without alignments)  
681.481 Million cell updates/sec

Title: US-10-660-357A-10  
Perfect score: 566  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QSYSTPPESFGQGTKLEIK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues  
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	566	100.0	109	14	US-10-330-613-10
2	566	100.0	109	14	US-10-330-530-10
3	566	100.0	109	16	US-10-660-357-10
4	520	91.9	108	17	US-10-726-332-214
5	520	91.9	108	17	US-10-805-177-64
6	519	91.7	108	17	US-10-726-332-18
7	517	90.3	108	17	US-10-726-332-28
8	512	90.5	107	17	US-10-727-155-308
9	512	90.5	108	17	US-10-726-332-209
10	512	90.5	238	20	US-11-031-485-28
11	511	90.3	107	10	US-09-791-153A-67

12	511	90.3	108	16	US-10-409-814A-4	Sequence 4, Appli
13	511	90.3	108	17	US-10-805-177-20	Sequence 20, Appli
14	511	90.3	240	9	US-09-192-854-2	Sequence 2, Appli
15	511	90.3	240	9	US-09-968-561A-2	Sequence 2, Appli
16	511	90.3	240	10	US-09-968-744A-2	Sequence 2, Appli
17	511	90.3	240	11	US-09-968-561A-2	Sequence 2, Appli
18	511	90.3	240	16	US-10-744-774-1	Sequence 1, Appli
19	511	90.3	240	20	US-11-115-682-2	Sequence 22, Appli
20	509	89.9	108	17	US-10-726-332-22	Sequence 220, App
21	508.5	89.8	111	17	US-10-726-332-220	Sequence 22, App
22	508	89.8	111	18	US-10-916-840-100	Sequence 100, App
23	505.5	89.3	107	20	US-11-031-485-124	Sequence 124, App
24	505.5	89.3	108	20	US-09-848-798-32	Sequence 32, Appli
25	505.5	89.3	108	10	US-09-848-798-43	Sequence 43, Appli
26	505.5	89.3	111	17	US-10-726-332-221	Sequence 221, App
27	505	89.2	106	20	US-11-031-485-128	Sequence 128, App
28	505	89.2	111	14	US-10-203-754A-56	Sequence 56, Appli
29	504	89.0	108	16	US-10-744-774-15	Sequence 15, Appli
30	504	89.0	116	17	US-10-783-311-138	Sequence 138, App
31	502	88.7	107	15	US-10-309-762-88	Sequence 88, Appli
32	502	88.7	107	17	US-10-938-353-103	Sequence 103, App
33	501.5	88.6	108	10	US-09-848-798-167	Sequence 167, App
34	500	88.3	106	15	US-10-377-121-5	Sequence 5, Appli
35	500	88.3	108	14	US-10-125-687-8	Sequence 8, Appli
36	500	88.3	108	18	US-10-996-191-8	Sequence 8, Appli
37	499.5	88.3	107	15	US-10-363-349-4	Sequence 4, Appli
38	499.5	88.3	288	15	US-10-363-349-7	Sequence 7, Appli
39	499	88.2	107	14	US-10-016-986-105	Sequence 105, App
40	498	88.0	105	15	US-10-309-762-155	Sequence 155, App
41	498	88.0	107	14	US-10-016-986-104	Sequence 104, App
42	498	88.0	107	15	US-10-309-762-67	Sequence 67, Appli
43	498	88.0	107	15	US-10-309-762-68	Sequence 68, Appli
44	498	88.0	107	16	US-10-663-244-79	Sequence 79, Appli
45	498	88.0	107	17	US-10-949-135-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1  
US-10-330-613-10  
; Sequence 10, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX 022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-10

Query Match 100.0%; Score 566; DB 14; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.4e-38;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DIQMTQSPSSLSASVGRVTITCRASQISNLYNWYQQKFGKAPKLLIYGASSLQSGVPS	60
Db	1	DIQMTQSPSSLSASVGRVTITCRASQISNLYNWYQQKFGKAPKLLIYGASSLQSGVPS	60
Qy	61	RFSGSGSGTDFTLTITSLQPEDPATYCRQSYSTPPESFGQGTKLEIK	109
Db	61	RFSGSGSGTDFTLTITSLQPEDPATYCRQSYSTPPESFGQGTKLEIK	109

RESULT 2

```
US-10-330-530-10
; Sequence 10, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-10

Query Match          100.0%; Score 566; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.4e-38;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSTPPSCSFQGGTKLEIK 109

RESULT 3
US-10-660-357-10
; Sequence 10, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: AGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-10

Query Match          100.0%; Score 566; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.4e-38;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSTPPSCSFQGGTKLEIK 109

RESULT 4
US-10-726-332-214
; Sequence 214, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: AGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-214

Query Match          91.9%; Score 520; DB 17; Length 108;
Best Local Similarity 93.6%; Pred. No. 1.2e-34;
Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSTPPSCSFQGGTKLEIK 109
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSTPP--TFQGGTKVEIK 107

RESULT 5
US-10-805-177-64
; Sequence 64, Application US/10805177
; Publication No. US2005008449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Foltz, Ian
; APPLICANT: Tse, Kam Fai
; APPLICANT: Jeffers, Michael
; APPLICANT: Mesri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khramtsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
; FILE REFERENCE: ABXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-64

Query Match          91.9%; Score 520; DB 17; Length 108;
Best Local Similarity 93.6%; Pred. No. 1.2e-34;
Matches 102; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYGASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISYLNWYQOKPGKAPKLLIYAASSLSQSGVPS 60
```



Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSYTPPCECSFGQGTKEIK 109  
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

## RESULT 6

US-10-726-332-18  
; Sequence 18, Application US/10726332  
; Publication No. US20050058649A1  
; GENERAL INFORMATION:  
; APPLICANT: Gregory M. Landes  
; APPLICANT: Mary Haak-Frendscho  
; APPLICANT: Ling Chen  
; APPLICANT: Yen-Wah R. Lee  
; APPLICANT: Meina Liang  
; APPLICANT: Xiao-Feng  
; APPLICANT: Xiao-Chi Jia  
; APPLICANT: Mark R. Nocerini  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2  
; FILE REFERENCE: ABGENIX.072A  
; CURRENT APPLICATION NUMBER: US/10726.332  
; CURRENT FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: n/a  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 222  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-726-332-18

Query Match 91.7%; Score 519; DB 17; Length 108;  
Best Local Similarity 93.6%; Pred. No. 1.5e-34;  
Matches 102; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQGVPS 60  
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSYTPPCECSFGQGTKEIK 109  
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

## RESULT 7

US-10-726-332-28  
; Sequence 28, Application US/10726332  
; Publication No. US20050058649A1  
; GENERAL INFORMATION:  
; APPLICANT: Gregory M. Landes  
; APPLICANT: Mary Haak-Frendscho  
; APPLICANT: Ling Chen  
; APPLICANT: Yen-Wah R. Lee  
; APPLICANT: Meina Liang  
; APPLICANT: Xiao-Feng  
; APPLICANT: Xiao-Chi Jia  
; APPLICANT: Mark R. Nocerini  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2  
; FILE REFERENCE: ABGENIX.072A  
; CURRENT APPLICATION NUMBER: US/10726.332  
; CURRENT FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: n/a  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 222  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-726-332-28

Query Match 91.3%; Score 517; DB 17; Length 108;  
Best Local Similarity 92.7%; Pred. No. 2.1e-34;  
Matches 101; Conservative 5; Mismatches 1; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQGVPS 60  
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSYTPPCECSFGQGTKEIK 109  
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTPP--TFGQGTKEIK 107

## RESULT 8

US-10-727-155-308  
; Sequence 308, Application US/10727155  
; Publication No. US20050049402A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaspal S. Kang  
; APPLICANT: Orit Foord  
; APPLICANT: Larry Green  
; APPLICANT: Xiao-Feng  
; APPLICANT: Scott Kiakamp  
; APPLICANT: Mary Haak-Frendscho  
; APPLICANT: Palaniswami Rathanaswami  
; APPLICANT: Craig Pigott  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Manchulenchao  
; APPLICANT: Raffaella Faggioni  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Qiaojuan Jane Su  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
; FILE REFERENCE: ABGENIX.073A  
; CURRENT APPLICATION NUMBER: US/10727.155  
; CURRENT FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: 60/430729  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 320  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 308  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-727-155-308

Query Match 90.5%; Score 512; DB 17; Length 107;  
Best Local Similarity 92.7%; Pred. No. 5.3e-34;  
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYGASSLSQGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQISNYLNWYQKPGKAPKLLIYAASSLSQGVPS 60  
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSYTPPCECSFGQGTKEIK 109  
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTPP--ITFGQGTKEIK 107

## RESULT 9

US-10-726-332-209  
; Sequence 209, Application US/10726332  
; Publication No. US20050058649A1  
; GENERAL INFORMATION:  
; APPLICANT: Gregory M. Landes  
; APPLICANT: Mary Haak-Frendscho  
; APPLICANT: Ling Chen  
; APPLICANT: Yen-Wah R. Lee  
; APPLICANT: Meina Liang  
; APPLICANT: Xiao-Feng

; APPLICANT: Xiao-Chi Jia  
; APPLICANT: Mark R. Nocerini  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2  
; FILE REFERENCE: ABGENIX 072A  
; CURRENT APPLICATION NUMBER: US/10/726,332  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR FILING DATE: n/a  
; NUMBER OF SEQ ID NOS: 222  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 209  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-726-332-209

Query Match 90.5%; Score 512; DB 17; Length 108;  
Best Local Similarity 92.7%; Pred. No. 5.4e-34;  
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTTTCRASQSIISYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGDRTTTCRASQSIISYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSTPPSCSFGQGTKEIK 109  
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTP--ITFGQGTKEIK 107

RESULT 10  
US-11-031-485-28  
; Sequence 28, Application US/11031485  
; Publication No. US20050232917A1  
; GENERAL INFORMATION:  
; APPLICANT: PULLEN, NICHOLAS  
; APPLICANT: MOLLOY, ELIZABETH  
; APPLICANT: KELLERMAN, SIRID-AIMEE  
; APPLICANT: GREEN, LARRY L.  
; APPLICANT: HAAK-FRENDSCHO, MARY  
; TITLE OF INVENTION: ANTIBODIES TO MADCAM  
; FILE REFERENCE: ABX-PF6  
; CURRENT APPLICATION NUMBER: US/11/031.485  
; CURRENT FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: 60/535,490  
; PRIOR FILING DATE: 2004-01-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 28  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-031-485-28

Query Match 90.5%; Score 512; DB 20; Length 238;  
Best Local Similarity 89.0%; Pred. No. 1.1e-33;  
Matches 97; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTTTCRASQSIISYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60  
Db 23 DIQWTQSPSSLSASVGDRTTTCRASQSIISYLNWYQKPGKAPKLLIYAASSLPRGVPS 82  
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSTPPSCSFGQGTKEIK 109  
Db 83 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYNNPPECGFGQGTLDIK 131

RESULT 11  
US-09-791-153A-67  
; Sequence 67, Application US/09791153A  
; Publication No. US20030103978A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra

; APPLICANT: Hitz, Anna  
; APPLICANT: Boyle, William  
; APPLICANT: Sullivan, John  
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN  
; FILE REFERENCE: A-633A  
; CURRENT APPLICATION NUMBER: US/09/791,153A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/511,139  
; PRIOR FILING DATE: 2000-02-23  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 67  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-153A-67

Query Match 90.3%; Score 511; DB 10; Length 107;  
Best Local Similarity 92.7%; Pred. No. 6.4e-34;  
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTTTCRASQSIISYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGDRTTTCRASQSIISYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSTPPSCSFGQGTKEIK 109  
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTP--WTFGQGTKEIK 107

RESULT 12  
US-10-409-814A-4  
; Sequence 4, Application US/10409814A  
; Publication No. US20040202995A1  
; GENERAL INFORMATION:  
; APPLICANT: de Wildt, Rudolf  
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND SCREENING METHODS  
; FILE REFERENCE: 8039/2032  
; CURRENT APPLICATION NUMBER: US/10/409,814A  
; CURRENT FILING DATE: 2003-04-09  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-409-814A-4

Query Match 90.3%; Score 511; DB 16; Length 108;  
Best Local Similarity 92.7%; Pred. No. 6.4e-34;  
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTTTCRASQSIISYLNWYQKPGKAPKLLIYGASSLSQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGDRTTTCRASQSIISYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTDTLTITSSLOPEDFATYYCROSYSTPPSCSFGQGTKEIK 109  
Db 61 RFGSGSGTDTLTITSSLOPEDFATYYCQOSYSTPN--TFGQGTKEIK 107

RESULT 13  
US-10-805-177-20  
; Sequence 20, Application US/10805177  
; Publication No. US2005008449A1  
; GENERAL INFORMATION:  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Chen, Francine  
; APPLICANT: Bezabeh, Binyam  
; APPLICANT: Foltz, Ian  
; APPLICANT: Tse, Kam Fai  
; APPLICANT: Jeffers, Michael  
; APPLICANT: Mesri, Mehdi

```
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Kiramtssov, Nikolia
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIN-1) ANTIGEN AND USES THEREOF
; FILE REFERENCE: ABXCUR 006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-20

Query Match          90.3%; Score 511; DB 17; Length 108;
Best Local Similarity 91.7%; Pred. No. 6.4e-34;
Matches 100; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSLASVGDVRVTITCRASQISNYLNWYQKPKAPKLLIYGASSIQQSGVPS 60
Db 1 DIQWTQSPSLASVGDVRVTITCRASQISNYLNWYQKPKAPKLLIYAASSIQQSGVPS 60

Qy 61 RFGSGSGTDFTLTISSLOPEDFATYYCROSYSPTPECSFGQGTKEIK 109
Db 61 RFGSGSGTDFTLTISSLOPEDFATYYCQOSYSTPN--TFGQGTKEIK 107

RESULT 14
US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2

Query Match          90.3%; Score 511; DB 9; Length 240;
Best Local Similarity 92.7%; Pred. No. 1.4e-33;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSLASVGDVRVTITCRASQISNYLNWYQKPKAPKLLIYGASSIQQSGVPS 60
Db 133 DIQWTQSPSLASVGDVRVTITCRASQISNYLNWYQKPKAPKLLIYAASSIQQSGVPS 192

Qy 61 RFGSGSGTDFTLTISSLOPEDFATYYCROSYSPTPECSFGQGTKEIK 109
Db 193 RFGSGSGTDFTLTISSLOPEDFATYYCQOSYSTPN--TFGQGTKEIK 239

RESULT 15
US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
```

```
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match          90.3%; Score 511; DB 9; Length 240;
Best Local Similarity 92.7%; Pred. No. 1.4e-33;
Matches 101; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSLASVGDVRVTITCRASQISNYLNWYQKPKAPKLLIYGASSIQQSGVPS 60
Db 133 DIQWTQSPSLASVGDVRVTITCRASQISNYLNWYQKPKAPKLLIYAASSIQQSGVPS 192

Qy 61 RFGSGSGTDFTLTISSLOPEDFATYYCROSYSPTPECSFGQGTKEIK 109
Db 193 RFGSGSGTDFTLTISSLOPEDFATYYCQOSYSTPN--TFGQGTKEIK 239

Search completed: November 16, 2005, 23:05:40
Job time : 66.9228 secs
```

THE MARCH 1978 (1978)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-14

Perfect score: 555

Sequence: 1 DIQWTSPLSASVGRVT.....CLOHNSYPLTFGGGTVKEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	107	7	Adc99785 Anti-huma
2	555	100.0	107	7	Add05389 Anti-MUC1
3	555	100.0	107	7	Adf09827 Human ant
4	555	100.0	107	7	Adk18843 Anti-huma
5	555	100.0	107	7	Adk18861 Anti-huma
6	555	100.0	107	7	Adk18594 Anti-huma
7	555	100.0	107	7	Adk18809 Anti-huma
8	555	100.0	107	7	Adp03911 Murine-ex
9	555	100.0	107	8	Adl25406 Human mAb
10	555	100.0	107	8	Adp23399 Human ant
11	555	100.0	107	8	Adp22314 Human ant
12	555	100.0	107	8	Adp22367 Human ant
13	555	100.0	107	8	Adp22302 Human ant
14	552	99.5	107	8	Adp22098 Human ant
15	552	99.5	107	8	Adp22122 Human ant
16	551	99.3	107	7	Adk18590 Anti-huma
17	551	99.3	107	7	Adk18839 Anti-huma
18	551	99.3	107	7	Adk18805 Anti-huma
19	551	99.3	107	8	Adl25398 Human mAb
20	551	99.3	107	8	Adp22318 Human ant
21	548	98.7	107	7	Adp03917 Murine-ex
22	548	98.7	107	8	Adp22102 Human ant
23	547	98.6	107	8	Adp22106 Human ant
24	546	98.4	107	8	Adp22220 Human ant
25	546	98.4	107	8	Adp22126 Human ant

26	544	98.0	107	7	Adp03918	Adp03918 Murine-ex
27	544	98.0	107	8	AdS84418	AdS84418 Human ant
28	544	98.0	107	8	AdR68560	AdR68560 Anti-EPO-
29	544	98.0	234	8	AdS84476	AdS84476 Human ant
30	544	98.0	234	8	AdR68618	AdR68618 Human ant
31	543	97.8	107	8	AdP22350	AdP22350 Human ant
32	543	97.8	110	5	RAU81280	RAU81280 Human trk
33	542	97.7	107	8	AdP22134	AdP22134 Human ant
34	542	97.7	107	8	AdP22138	AdP22138 Human ant
35	542	97.7	107	8	AdP22172	AdP22172 Human ant
36	542	97.7	107	8	AdP22346	AdP22346 Human ant
37	541	97.5	107	7	AdC99789	AdC99789 Anti-huma
38	541	97.5	107	7	AdD05393	AdD05393 Anti-MUC1
39	541	97.5	107	7	AdF09831	AdF09831 Human ant
40	541	97.5	107	7	AdK18842	AdK18842 Anti-huma
41	541	97.5	107	7	AdK18916	AdK18916 Anti-huma
42	541	97.5	107	7	AdK18892	AdK18892 Anti-huma
43	541	97.5	107	7	AdK18612	AdK18612 Anti-huma
44	541	97.5	107	7	AdK18602	AdK18602 Anti-huma
45	541	97.5	107	7	AdK18810	AdK18810 Anti-huma

#### ALIGNMENTS

##### RESULT 1

AdC99785

ID AdC99785 standard; protein; 107 AA.

XX AdC99785;

XX AdC99785;

DT 01-JAN-2004 (first entry)

XX AdC99785;

DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 14.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human.

XX Homo sapiens.

XX W02003057838-A2.

PN W02003057838-A2.

XX 17-JUL-2003.

PD 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

PF 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

PR 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

PA (ABGE-) ABGENIX INC.

XX Gudas J;

PI Gudas J;

XX WPI; 2003-587113/55.

XX N-PSDB; AdC99787.

DR New human anti-MUC18 monoclonal antibodies, useful for treating a disease

XX or condition associated with expression of MUC18 in a patient, e.g.

PT tumors, cancers, and other malignancies.

XX Claim 3; SEQ ID NO 14; 78pp; English.

PS The invention relates to a novel isolated monoclonal antibody comprising

XX a heavy or light chain amino acid or a heavy or light chain variable

XX domain where the antibody binds to MUC18. The monoclonal antibody of the

CC invention demonstrates cytostatic activity and may be useful for treating

CC a disease or condition associated with the expression of MUC18 on the

CC cell surface such as tumours, specifically melanoma, oesophageal,

CC pancreatic or colorectal tumours, carcinomas, particularly cervical

CC carcinomas and cervical intraepithelial neoplasia and cancers including

CC colorectal, breast or lung cancer, as well as other malignancies. The

CC current sequence is that of the anti-human MUC18 monoclonal antibody

```
CC light chain protein of the invention.
SQ Sequence 107 AA;

Query Match      100.0%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 9.2e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPLTFGGGTKVEIK 107

RESULT 2
ADD05389
ID ADD05389 standard; protein; 107 AA.
XX
AC ADD05389;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 14.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
WPI: 2003-577496/54.
DR N-PSDB; ADD05391.
XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 3; SEQ ID NO 14; 87pp; English.
XX
SS The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 9.2e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPLTFGGGTKVEIK 107

RESULT 3
ADF09827
ID ADF09827 standard; protein; 107 AA.
XX
AC ADF09827;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #4.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI: 2003-598367/56.
DR N-PSDB; ADF09829.
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumour
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 3; SEQ ID NO 14; 83pp; English.
XX
SS The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 9.2e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLPQEDFATYYCLOHNSYPLTFGGGTKVEIK 107
```



PA (ABGE-) ABGENIX INC.  
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX WPI; 2003-587119/55.  
XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX Disclosure; SEQ ID NO 18; 255pp; English.  
XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX Sequence 107 AA;  
XX Query Match 100.0%; Score 555; DB 7; Length 107;  
XX Best Local Similarity 100.0%; Pred. No. 9.2e-35;  
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
Oy 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107  
Db 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107  
RESULT 7  
ADK18809  
ID ADK18809 standard; protein; 107 AA.  
XX ADK18809;  
XX 06-MAY-2004 (first entry)  
XX Anti-human PDGF-D antibody protein related sequence #35.  
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
XX Homo sapiens.  
XX WO2003057857-A2.  
XX 17-JUL-2003.  
XX 06-JAN-2003; 2003WO-US0000398.  
XX 07-JAN-2002; 2002US-00041860.  
XX (ABGE-) ABGENIX INC.  
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX WPI; 2003-587119/55.  
XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX Disclosure; SEQ ID NO 233; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX Sequence 107 AA;  
XX Query Match 100.0%; Score 555; DB 7; Length 107;  
XX Best Local Similarity 100.0%; Pred. No. 9.2e-35;  
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
Oy 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107  
Db 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107  
RESULT 8  
ADP03911  
ID ADP03911 standard; protein; 107 AA.  
XX ADP03911;  
XX 29-JUL-2004 (first entry)  
XX Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 51.  
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX cytostatic; colorectal neoplasm; renal cell carcinoma;  
XX cervical intraepithelial squamous neoplasia;  
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX gene therapy; murine; mouse; human; light chain variable domain.  
XX Unidentified.  
XX WO2003048328-A2.  
XX 12-JUN-2003.  
XX 02-DEC-2002; 2002WO-US038550.  
XX 03-DEC-2001; 2001US-0337275P.  
XX (ABGE-) ABGENIX INC.  
PI Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX Claim 3; SEQ ID NO 51; 89pp; English.  
XX The invention relates to a novel isolated monoclonal antibody (mAb)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX demonstrates cytostatic activity and may be useful for treating a tumour,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal



CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VL  
CC (light chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9.2e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLQWYQKPKAPKRLIYAASLSQGVPS 60

Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLQWYQKPKAPKRLIYAASLSQGVPS 60

Qy 61 RFGSGSGTEFTLTISLQPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

Db 61 RFGSGSGTEFTLTISLQPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

RESULT 9

ADL25406

ID ADL25406 standard; protein; 107 AA.

XX AC ADL25406;

XX DT 17-JUN-2004 (first entry)

XX DE Human mAb 1.17 light chain variable region protein SEQ ID NO:16.

XX KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;

XX KW nephritis; mesangial cell proliferation inhibition;

XX KW mesangial proliferative glomerulonephritis; nephrotropic;

XX KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;

XX KW gene therapy; human; monoclonal antibody; mAb.

XX OS Homo sapiens.

XX WO2004024098-A2.

XX PD 25-MAR-2004.

XX PF 16-SEP-2003; 2003WO-US029414.

XX PR 16-SEP-2002; 2002US-0411137P.

XX PA (ABGE-) ABGENIX INC.

XX PA (CURA-) CURAGEN CORP.

XX PI Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;

XX DR WPI; 2004-269881/25.

XX DR N-PSDB; ADL25405.

XX PT Use of an antibody or its binding fragment that binds platelet derived  
XX growth factor-DD (PDGF-DD) for preparing a medicament for treating  
XX nephritis.

XX PS Disclosure; SEQ ID NO 16; 115pp; English.

XX CC The present invention describes an antibody or its binding fragment that  
XX binds platelet derived growth factor-DD (PDGF-DD), where the antibody is  
XX useful in preparing a medicament for treating nephritis. Also described:  
XX (1) a method of detecting nephritis; (2) a method of treating nephritis;  
XX (3) a method of inhibiting mesangial cell proliferation; and (4) a method  
XX of treating mesangial proliferative glomerulonephritis. The antibody has  
XX nephrotropic, antiinflammatory, dermatological, immunosuppressive and  
XX antidiabetic activities, and can be used in gene therapy. The antibody or  
XX its binding fragment, that binds PDGF-DD, can be used in preparing a  
XX medicament for treating nephritis and related disorders, e.g., mesangial  
XX proliferative glomerulonephritis. The present sequence represents a human  
XX monoclonal antibody (mAb) variable region sequence, which is used in the

CC exemplification of the present invention.

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 555; DB 8; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9.2e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLQWYQKPKAPKRLIYAASLSQGVPS 60

Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLQWYQKPKAPKRLIYAASLSQGVPS 60

Qy 61 RFGSGSGTEFTLTISLQPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

Db 61 RFGSGSGTEFTLTISLQPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

RESULT 10

ADP22399

ID ADP22399 standard; protein; 107 AA.

XX AC ADP22399;

XX DT 09-SEP-2004 (first entry)

XX DE Human anti-TNFA antibody light chain variable region SEQ ID NO:305.

XX KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;

XX KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;

XX KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;

XX KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;

XX KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;

XX KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;

XX KW bladder cancer; lung cancer; glioblastoma; stomach cancer;

XX KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;

XX KW prostrate cancer; immuno-mediated inflammatory disease;

XX KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;

XX KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;

XX KW septic shock; cachexia; anorexia; multiple sclerosis.

XX OS Homo sapiens.

XX WO2004050683-A2.

XX PD 17-JUN-2004.

XX PF 02-DEC-2003; 2003WO-US038281.

XX PR 02-DEC-2002; 2002US-0430729P.

XX PA (ABGE-) ABGENIX INC.

XX PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

XX PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;

XX PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;

XX DR WPI; 2004-480601/45.

XX PT New recombinant human monoclonal antibody that specifically binds to  
XX Tumor Necrosis Factor-alpha, useful for treating neoplastic diseases such  
XX as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
XX arthritis.

XX PS Example 10; SEQ ID NO 305; 213pp; English.

XX CC The present invention describes a human monoclonal antibody (I) that  
XX specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
XX (a) a heavy chain complementarity determining region 1 (CDR1) having the  
XX two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
XX and (b) a light chain CDR1 having the two fully defined 11 amino acid  
XX sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
XX (MI) the level of TNFA in a patient sample, comprising contacting with  
XX (I), and detecting the level of binding between the antibody and TNFA in

CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFa induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC stomach cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody light chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 8; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-35;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60  
 Db 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107

Db 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107

RESULT 11

ID ADP22314 standard; protein; 107 AA.

XX AC ADP22314;

XX DT 09-SEP-2004 (first entry)

XX DE Human anti-TNFA antibody light chain variable region SEQ ID NO:220.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.

XX OS Homo sapiens.

XX PN W02004050683-A2.

XX PD 17-JUN-2004.

XX PF 02-DEC-2003; 2003WO-US038281.

XX PR 02-DEC-2002; 2002US-0430729P.

XX PA (ABGE-) ABGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulchenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX WPI; 2004-480601/45.  
 DR N-PSDB; ADP22313.

XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.

XX Example 10; SEQ ID NO 220; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFA in a patient sample, comprising contacting with  
 CC (I), and detecting the level of binding between the antibody and TNFA in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFA induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody light chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 8; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-35;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60  
 Db 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107

Db 61 RFSGSGSGTFTLTISLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107

RESULT 12

ID ADP22367 standard; protein; 107 AA.

XX AC ADP22367;

XX DT 09-SEP-2004 (first entry)

XX DE Human anti-TNFA antibody light chain variable region SEQ ID NO:273.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;

eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 neuroprotective; vasotropic; antiapoptotic; TNF antagonist;  
 TNF induced apoptosis; neoplastic disease; breast cancer;  
 bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 prostate cancer; immuno-mediated inflammatory disease;  
 rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 septic shock; cachexia; anorexia; multiple sclerosis.  
 Homo sapiens.  
 WO2004050683-A2.  
 17-JUN-2004.  
 02-DEC-2003; 2003WO-US038281.  
 02-DEC-2002; 2002US-0430729P.  
 (ABGE-) ABGENIX INC.  
 Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;  
 Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 WPI; 2004-480601/45.  
 New recombinant human monoclonal antibody that specifically binds to  
 Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 arthritis.  
 Example 10; SEQ ID NO 273; 213pp; English.  
 The present invention describes a human monoclonal antibody (I) that  
 specifically binds to tumour necrosis factor-alpha (TNF) and comprises:  
 (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 (M1) the level of TNF in a patient sample, comprising contacting with  
 the sample; (2) a composition comprising the antibody and TNF in  
 the sample; (3) treating (M2) an animal suffering from a  
 fragment and a carrier; (4) inhibiting (M3) TNF induced  
 apoptosis in an animal by selecting an animal in need of treatment for  
 TNF induced apoptosis by administering the human monoclonal antibody of  
 (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 antidiabetic, antinflammatory, antipapillary, antipneumatic, eating-  
 disorders, immunomodulator, immunosuppressive, nephrotropic,  
 neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 as a TNF antagonist. The antibody (I) is useful in the preparation of  
 medicament for treating TNF induced apoptosis, neoplastic disease such as  
 breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 diseases such as rheumatoid arthritis, glomerulonephritis,  
 atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 multiple sclerosis. The present sequence represents a human anti-TNFA  
 antibody light chain variable region, which is used in the  
 exemplification of the present invention.  
 Query Match  
 Best Local Similarity 100.0%; Score 555; DB 8; Length 107;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 DIQWTSPLSASVGRVITTCRASQGIKNDLGMVQKPKAPKRIIYAASSLSQGVPS 60

Db 1 DIQWTSPLSASVGRVITTCRASQGIKNDLGMVQKPKAPKRIIYAASSLSQGVPS 60  
 Qy 61 RFGSGSGTEFTLTISLQPEDFATYVCLQHSYPLTFGGTKVEIK 107  
 Db 61 RFGSGSGTEFTLTISLQPEDFATYVCLQHSYPLTFGGTKVEIK 107  
 RESULT 13  
 ADP22302  
 ID ADP22302 standard; protein; 107 AA.  
 AC ADP22302;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human anti-TNFA antibody light chain variable region SEQ ID NO:208.  
 XX  
 KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antinflammatory; antipapillary; antipneumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNF antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004050683-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038281.  
 XX  
 PR 02-DEC-2002; 2002US-0430729P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX  
 DR WPI; 2004-480601/45.  
 DR N-PSDB; ADP22301.  
 XX  
 PT New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 PS Example 10; SEQ ID NO 208; 213pp; English.  
 XX  
 CC The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNF in a patient sample, comprising contacting with  
 CC the sample; (2) a composition comprising the antibody and TNFA in  
 CC the sample; (3) treating (M2) an animal suffering from a  
 CC fragment and a carrier; (4) inhibiting (M3) TNF induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNF induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antidiabetic, antinflammatory, antipapillary, antipneumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody light chain variable region, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 107 AA;

CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody light chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 555; DB 8; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-35;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIQQTSPSSLSASVGDRTVITCRASQIRNDLGWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQQTSPSSLSASVGDRTVITCRASQIRNDLGWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Oy 61 RFGSGSGTFTLTISLQPEDFATYICLOHNSVPLTFGGTKVEIK 107

Db 61 RFGSGSGTFTLTISLQPEDFATYICLOHNSVPLTFGGTKVEIK 107

RESULT 14

ADP22098

ID ADP22098 standard; protein; 107 AA.

XX ADP22098;

XX 09-SEP-2004 (first entry)

XX Human anti-TNFA antibody light chain variable region SEQ ID NO:4.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.

XX WO2004050683-A2.

XX 17-JUN-2004.

XX 02-DEC-2003; 2003WO-US038281.

XX 02-DEC-2002; 2002US-0430729P.

XX (ABGE-) ABGENIX INC.

XX Babcock JS, Kang JS, Foord O, Green L, Peng X, Klakamp S;

PI Haak-Frendscho M, Rathanaasami P, Pigott C, Liang ML, Lee R;

PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;

XX WPI; 2004-480601/45.

DR N-PSDB; ADP22097.

XX New recombinant human monoclonal antibody that specifically binds to

PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.

XX Example 10; SEQ ID NO 4; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDRI) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDRI having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC the level of TNFA in a patient sample, comprising contacting with  
 CC (I), and detecting the level of binding between the antibody and TNFA in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFA induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody light chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 99.5%; Score 552; DB 8; Length 107;

Best Local Similarity 99.1%; Pred. No. 1.6e-34;

Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIQQTSPSSLSASVGDRTVITCRASQIRNDLGWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQQTSPSSLSASVGDRTVITCRASQIRNDLGWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Oy 61 RFGSGSGTFTLTISLQPEDFATYICLOHNSVPLTFGGTKVEIK 107

Db 61 RFGSGSGTFTLTISLQPEDFATYICLOHNSVPLTFGGTKVEIK 107

RESULT 15

ADP22122

ID ADP22122 standard; protein; 107 AA.

XX ADP22122;

XX 09-SEP-2004 (first entry)

XX Human anti-TNFA antibody light chain variable region SEQ ID NO:28.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;

septic shock; cachexia; anorexia; multiple sclerosis.

Search completed: November 16, 2005, 21:51:38

Job time : 62.3676 secs

Homo sapiens.

WO2004050683-A2.

17-JUN-2004.

02-DEC-2003; 2003WO-US038281.

02-DEC-2002; 2002US-0430729P.

(ABGE-) ABGENIX INC.

Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;

Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;

WPI; 2004-480601/45.

DR N-PSDB; ADP22121.

New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor- $\alpha$ , useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid arthritis.

Example 10; SEQ ID NO 28; 213pp; English.

The present invention describes a human monoclonal antibody (I) that specifically binds to tumour necrosis factor- $\alpha$  (TNF $\alpha$ ) and comprises: (a) a heavy chain complementarity determining region 1 (CDRI) having the two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421); and (b) a light chain CDRI having the two fully defined 11 amino acid sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying (M1) the level of TNF $\alpha$  in a patient sample, comprising contacting with (I), and detecting the level of binding between the antibody and TNF $\alpha$  in the sample; (2) a composition comprising the antibody or its functional fragment and a carrier; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human monoclonal antibody of (I); and (4) inhibiting (M3) TNF $\alpha$  induced apoptosis in an animal by selecting an animal in need of treatment for TNF $\alpha$  induced apoptosis by administering the human monoclonal antibody of (I). (I) has anabolic, antiarteriosclerotic, antiarthritic, antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-disorders, immunomodulator, immunosuppressive, nephrotropic, neuroprotective, vasotropic and antiapoptotic activities, and can be used as a TNF $\alpha$  antagonist. The antibody (I) is useful in the preparation of medicament for treating TNF induced apoptosis, neoplastic disease such as breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, kidney cancer, colon cancer, pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory diseases such as rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence represents a human anti-TNF $\alpha$  antibody light chain variable region, which is used in the exemplification of the present invention.

Sequence 107 AA;

Query Match 99.5%; Score 552; DB 8; Length 107;  
Best Local Similarity 99.1%; Pred. No. 1.6e-34;  
Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGIKNDLQWYQKFKAPKRLIYAASLSQGVPS 60

Db 1 DIQWTQSPSSLSASVGRVITTCRASQGIKNDLQWYQKFKAPKRLIYAASLSQGVPS 60

Qy 61 RFGSGSGSTFTLTITSSLPQEDPATYTCLOHNSVPLTFGGGTVK 107

Db 61 RFGSGSGSTFTLTITSSLPQEDPATYTCLOHNSVPLTFGGGTVK 107

THIS PAGE IS BLANK (CBPTD)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-14

Perfect score: 555

Sequence: 1 DIQMTQSPSSLSASVGDRTV.....CLQHNSTPLTFGGGTVKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	537	96.8	125	2 S40353	Ig kappa chain V-J
2	505	91.0	123	2 S40313	Ig kappa chain V-J
3	504	90.8	108	1 KIHUGL	Ig kappa chain V-I
4	503	90.6	107	2 S36269	Ig lambda chain V
5	501	90.3	108	1 KIHUWE	Ig kappa chain V-I
6	497	89.5	107	2 S36262	Ig lambda chain V
7	494	89.0	117	2 S41809	Ig kappa chain V r
8	493	88.8	108	2 S36279	Ig lambda chain V
9	486	87.6	114	2 S46377	Ig kappa chain V-J
10	484	87.2	125	2 S40349	Ig kappa chain V-J
11	481	86.7	108	2 B49047	Ig kappa chain V r
12	480	86.5	132	2 S40334	Ig kappa chain - h
13	476	85.8	107	2 S36264	Ig lambda chain V
14	475	85.6	108	2 S19674	Ig kappa chain V r
15	475	85.6	125	2 S40333	Ig kappa chain V-J
16	475	85.6	129	2 S40369	Ig kappa chain - h
17	470	84.7	126	2 S40335	Ig kappa chain V-J
18	467	84.1	95	2 S69898	Ig kappa chain V r
19	467	84.1	123	2 S40331	Ig kappa chain - h
20	466	84.0	129	2 S52793	Ig kappa chain V r
21	465	83.8	127	2 S40367	Ig kappa chain V-J
22	464	83.6	108	2 S36277	Ig lambda chain V
23	463	83.4	131	2 S40352	Ig kappa chain V-J
24	462	83.2	125	2 S40316	Ig kappa chain - h
25	461.5	83.2	124	2 S40336	Ig kappa chain V-J
26	461	83.1	105	2 S36266	Ig lambda chain V
27	461	83.1	107	2 I69017	anti-HIV1 envelope
28	460	82.9	129	2 S52789	Ig kappa chain V r
29	459	82.7	129	2 S40317	Ig kappa chain - h

## ALIGNMENTS

### RESULT 1

S40353

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40353

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40353

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72463

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 96.8%; Score 537; DB 2; Length 125;

Best Local Similarity 96.3%; Pred. No. 3.4e-39;

Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGNDLQWYQKPGKAPKRLIYAASLSQSGVPS 60

Db 15 DIQMTQSPSSLSASVGDRTVITCRASQIGNDLQWYQKPGKAPKRLIYAASLSQSGVPS 74

QY 61 RPSGSGSGTFTLTISLQPEDFATYYCLQHNSTPLTFGGGTVKVEIK 107

Db 75 RPSGSGSGTFTLTISLQPEDFATYYCLQHNSTPLTFGGGTVKVEIK 121

### RESULT 2

S40313

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40313

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40313

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:Cross-references: EMBL:X72423; NID:g441314; PIDN:CAAS1091.1; PID:g441315

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 91.0%; Score 505; DB 2; Length 123;





```
QY 1 DIQWTSPLSASVGRVTTTCRASQIRNDLQWYQKPKAPKRLIYAASLSQGVPS 60
Db 1 DIWVTSPLSASIGRVRTTTCRESQIRNDLQWYQKPKAPKRLIYAASLSQGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSVPLTFGGGTVKEIK 107
Db 61 RFGSGSGTDTLTISLQPEDFATYCYCLOHNSVPLTFGGGTVKEIK 107

RESULT 7
S41809
Ig kappa chain V region A30 - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S41809
R;Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zae
Eur. J. Immunol. 23, 2868-2875, 1993
A:Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequen
A:Reference number: S41809; MUID:94039386; PMID:8223863
A:Accession: S41809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <HUB>
A:Cross-references: EMBL:X72808; NID:g415383; PIDN:CAA51328.1; PID:g415384
C:Genetics: 19/1
A:Introns: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 494; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGRVTTTCRASQIRNDLQWYQKPKAPKRLIYAASLSQGVPS 60
Db 23 DIQWTSPLSASVGRVTTTCRASQIRNDLQWYQKPKAPKRLIYAASLSQGVPS 82

QY 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSYP 95
Db 83 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSYP 117

RESULT 8
S36279
Ig lambda chain V region (Clone alpha-THY-23) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36279
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Enbleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36279; MUID:93178448; PMID:7679990
A:Accession: S36279
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <GR1>
A:Cross-references: EMBL:Z18831; NID:g33418; PIDN:CAA79283.1; PID:g939911
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 88.8%; Score 493; DB 2; Length 108;
Best Local Similarity 88.8%; Pred. No. 1.7e-35;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGRVTTTCRASQIRNDLQWYQKPKAPKRLIYAASLSQGVPS 60
Db 1 DIQWTSPLSASVGRVTTTCRASQIRNDLQWYQKPKAPKRLIYAASLSQGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSVPLTFGGGTVKEIK 107
Db 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSVPLTFGGGTVKEIK 107
```

## RESULT 9

S46377

Ig kappa chain V-J region (T33-17) - human (fragment)

C:Species: Homo sapiens (man)

C&gt;Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C:Accession: S46377; S38650

R;Bensimon, C.; Chaetagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rear

A:Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46377

A:Molecule type: mRNA

A:Residues: 1-114 &lt;BEN&gt;

A:Cross-references: EMBL:Z27178; NID:g415971; PIDN:CAA81702.1; PID:g415972

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;22-96/Domain: immunoglobulin homology &lt;IMM&gt;

## RESULT 11

B49047

Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme

C:Species: Homo sapiens (man)

C&gt;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: B49047

R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.

Eur. J. Immunol. 22, 2231-2236, 1992

A;Title: Human monoclonal striatal autoantibodies isolated from thymic B lymphocytes  
A;Reference number: A49047; MUID:92387224; PMID:1516616  
A;Accession: B49047  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-108 <VIC>  
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77  
A;Experimental source: thymic B lymphocytes  
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIIP:113209)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 481; DB 2; Length 108;  
Best Local Similarity 89.7%; Pred. No. 1.8e-34;  
Matches 96; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
DB 1 DIQWTSPLSASVGDRTTTCRASQISISSYLNWYQKPGKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSYPLTFGGGTVKVEIK 107  
DB 61 RFGSGSGTDFLTITISLQPEDFATYCYCQSYSTPLTFGGGTVKVEIK 107

RESULT 12  
S40334  
Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40334  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40334  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-132 <KLE>  
A;Cross-references: EMBL:X72444  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 480; DB 2; Length 132;  
Best Local Similarity 86.0%; Pred. No. 2.7e-34;  
Matches 92; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
DB 22 DIQWTSPLSASVGDRTTTCRASQISYSLWYQKPGKAPKRLIYAASSLSQSGVPS 81

QY 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSYPLTFGGGTVKVEIK 107  
DB 82 RFGSGSGTDFLTITISLQPEDFATYCYCQSYSTPLTFGGGTVKVEIR 128

RESULT 13  
S36264  
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C;Accession: S36264  
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A;Title: Human anti-self antibodies with high specificity from phage display libraries.  
A;Reference number: S36256; MUID:93178448; PMID:7679990  
A;Accession: S36264  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-107 <GRI>  
A;Cross-references: EMBL:218845; NID:G33426; PIDN:CAA79297.1; PID:G939919  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.8%; Score 476; DB 2; Length 107;  
Best Local Similarity 86.0%; Pred. No. 4.8e-34;  
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
DB 1 EIVLTQSPSLSASVGDRTTTCRASQISISSYLNWYQKPGKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSYPLTFGGGTVKVEIK 107  
DB 61 RFGSGSGTDFLTITISLQPEDFATYCYCQSYSTPLTFGGGTVKDIK 107

RESULT 14  
S19674  
Ig kappa chain V region (clone alpha-TEL9) - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C;Accession: S19674  
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
A;Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on phage  
A;Reference number: S19663; MUID:92085276; PMID:1748994  
A;Accession: S19674  
A;Molecule type: mRNA  
A;Residues: 1-108 <MAR>  
A;Cross-references: EMBL:X61642; NID:G37860; PIDN:CAA3823.1; PID:G133386  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 475; DB 2; Length 108;  
Best Local Similarity 86.0%; Pred. No. 5.9e-34;  
Matches 92; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
DB 1 EIVLTQSPSLSASVGDRTTTCRASQISISSYLNWYQKPGKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSYPLTFGGGTVKVEIK 107  
DB 61 RFGSGSGTDFLTITISLQPEDFATYCYCQSYSTPLTFGGGTVKLEIK 107

RESULT 15  
S40333  
Ig kappa chain V-J region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40333  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40333  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-125 <KLE>  
A;Cross-references: EMBL:X72443; NID:G441354; PIDN:CAA51111.1; PID:G441355  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 475; DB 2; Length 125;  
Best Local Similarity 86.9%; Pred. No. 6.7e-34;  
Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
DB 19 DIQWTSPLSASVGDRTTTCRASQISISSYLNWYQKPGKAPKRLIYAASSLSQSGVPS 78

Search completed: November 16, 2005, 22:04:07  
Job time : 12.7849 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-14

Perfect score: 555

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLOHNSYPLTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : ..Uniprot 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	504	90.8	108	1 KV1G_HUMAN	P01599 homo sapien
2	501	90.3	108	1 KV1R_HUMAN	P01610 homo sapien
3	499	89.9	236	2 O6GMW1	O6GMW1 homo sapien
4	475	85.6	236	2 O6GMX8	O6GMX8 homo sapien
5	472	85.0	236	2 O6PIH7	O6PIH7 homo sapien
6	469	84.5	108	2 Q9UL70	Q9UL70 homo sapien
7	469	84.5	236	2 O6GMX9	O6GMX9 homo sapien
8	468	84.3	244	2 O65ZC8	O65ZC8 homo sapien
9	464.5	83.7	107	2 Q96SA9	Q96SA9 homo sapien
10	461	83.1	236	2 O6GMX0	O6GMX0 homo sapien
11	461	83.1	236	2 Q7Z3Y4	Q7Z3Y4 homo sapien
12	460	82.9	240	2 O65ZC9	O65ZC9 homo sapien
13	456	82.2	108	1 KV1V_HUMAN	P04430 homo sapien
14	454	81.8	108	2 Q9UL77	Q9UL77 homo sapien
15	452	81.4	108	1 KV1S_HUMAN	P01611 homo sapien
16	446	80.4	108	1 KV1H_HUMAN	P01600 homo sapien
17	445	80.2	108	1 KV1W_HUMAN	P80362 homo sapien
18	444	80.0	129	1 KV1W_HUMAN	P04431 homo sapien
19	441	79.5	108	1 KV1F_HUMAN	P01598 homo sapien
20	438.5	79.0	107	2 Q9UL81	Q9UL81 homo sapien
21	438	78.9	129	1 KV1X_HUMAN	P04432 homo sapien
22	438	78.9	236	2 O6PI75	O6PI75 homo sapien
23	437	78.7	108	1 KV1P_HUMAN	P01608 homo sapien
24	434	78.2	108	2 Q9UL79	Q9UL79 homo sapien
25	433	78.0	117	1 KV1I_HUMAN	P01601 homo sapien
26	432.5	77.9	107	1 KV1D_HUMAN	P01596 homo sapien
27	430	77.5	108	1 KV1B_HUMAN	P01594 homo sapien
28	430	77.5	108	1 KV1M_HUMAN	P01605 homo sapien
29	429	77.3	108	1 KV1L_HUMAN	P01604 homo sapien
30	428	77.1	108	1 KV1E_HUMAN	P01597 homo sapien
31	428	77.1	108	1 KV1Q_HUMAN	P01609 homo sapien

32	427	76.9	234	2 Q7Z473	Q7Z473 homo sapien
33	425	76.6	108	1 KV1O_HUMAN	P01607 homo sapien
34	424	76.4	236	2 Q6PIH4	Q6PIH4 homo sapien
35	423	76.2	108	1 KV1C_HUMAN	P01595 homo sapien
36	421	75.9	108	1 KV1N_HUMAN	P01606 homo sapien
37	420	75.7	108	1 KV1K_HUMAN	P01603 homo sapien
38	420	75.7	117	1 KV1J_HUMAN	P01602 homo sapien
39	413	74.4	108	1 KV1A_HUMAN	P01593 homo sapien
40	409	73.7	108	1 KV5S_MOUSE	P01652 mus musculus
41	409	73.7	116	2 Q96PF6	Q96PF6 homo sapien
42	408.5	73.6	109	1 KV1T_HUMAN	P01612 homo sapien
43	406	73.2	108	1 KV5Q_MOUSE	P01650 mus musculus
44	406	73.2	108	1 KV5T_MOUSE	P01653 mus musculus
45	396	71.4	108	1 KV5R_MOUSE	P01651 mus musculus

#### ALIGNMENTS

RESULT 1  
KV1G\_HUMAN STANDARD; PRT; 108 AA.  
ID KV1G\_HUMAN  
AC P01599;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-I region Gal.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
OX [1]  
RN MEDLINE=75059122; PubMed=4215718;  
RP Laure C.J., Watanabe S., Hilschmann N.;  
RA "The primary structure of a monoclonal IgM-immunoglobulin  
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of  
RT kappa-type, subgroup I."  
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenström's  
CC macroglobulin.  
DR PIR; A01867; KJHUGL.  
DR HSSP; P01607; 1BWV.  
GO: GO:0005576; C:extracellular; NAS.  
GO: GO:0003823; F:antigen binding; NAS.  
GO: GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.  
FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 90.8%; Score 504; DB 1; Length 108;  
Best Local Similarity 91.6%; Pred. No. 8.6e-44;  
Matches 39; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLIGWYQKPGKAPKRLIYAASLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTIIICRASQIGRNDLTWTYQKPGKAPKELIYAASNLQGVPS 60

QY 61 RFGSGSGTEFTTIISSLPEDFATYCYLQHNSYPLTFGGTKVEIK 107

Db 61 RFGSGGAGTEFTLTISLQPEDFATYVCLQNSYPRSGQGTKEIK 107

RESULT 2  
KVIR HUMAN STANDARD; PRT; 108 AA.  
AC P01610;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE IG kappa chain V-I region WEA.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83273707; PubMed=6410398;  
RA Goni F., Frangione B.;  
RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose  
RT in Klebsiella polysaccharides K30 and K33."  
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).  
CC -!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody  
CC against 3,4-pyruvylated galactose and isolated from a patient with  
CC Waldenstrom's macroglobulinemia.  
DR PIR; A01876; KIHWE.  
DR HSSP; P80362; LWTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region;  
KW Monoclonal antibody.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.  
FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;  
Query Match 90.3%; Score 501; DB 1; Length 108;  
Best Local Similarity 89.7%; Pred. No. 1.7e-43;  
Matches 96; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQIGRNDLGHYQKPGKAPKRLIYAASSLSQGVPS 60  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQIGRNDLGHYQKPGKAPKRLIYAASSLSQGVPS 60  
Qy 61 RFGSGGAGTEFTLTISLQPEDFATYVCLQNSYPLTFGGGTKEIK 107  
Db 61 RFGSGGAGTEFTLTISLQPEDFATYVCLQNSYPLTFGGGTKEIK 107

RESULT 3  
Q6GMW1 PRELIMINARY; PRT; 236 AA.  
AC Q6GMW1;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX Strausberg R.;  
RL EMBL; BC073791; AAH73791.1; -.  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-cl.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein  
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;  
Query Match 89.9%; Score 499; DB 2; Length 236;  
Best Local Similarity 92.5%; Pred. No. 6.8e-43;  
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
Qy 2 IQMTQSPSSLSASVGDRTVITCRASQIGRNDLGHYQKPGKAPKRLIYAASSLSQGVPSR 61  
Db 24 IQMTQSPSSLSASVGDRTVITCRASQIGRNDLGHYQKPGKAPKRLIYAASSLSQGVPSR 83  
Qy 62 FSGSGSGTEFTLTISLQPEDFATYVCLQNSYPLTFGGGTKEIK 107  
Db 84 FSGSGSGTEFTLTISLQPEDFATYVCLQNSYPLTFGGGTKEIK 129  
RESULT 4  
Q6GMX8 PRELIMINARY; PRT; 236 AA.  
AC Q6GMX8;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC073764; AAH73764.1; -  
 DR InterPro: IPR003599; Ig-like.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig v.  
 DR Pfam: PF07654; Cl-set; 1.  
 DR Pfam: PF00047; Ig; 2.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IG1; 1.  
 DR SMART: SM00406; IGv; 1.  
 DR PROSITE: PS50835; IG LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;  
 Query Match 85.6%; Score 475; DB 2; Length 236;  
 Best Local Similarity 86.9%; Pred. No. 1.9e-40;  
 Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 DIQWTPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASLSQGVPS 60  
 DB 23 DIQWTPSSVSVASVGRVITTCRASQISVSLAWYQKPKAPKRLIYAASLSQGVPS 82  
 QY 61 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYPLTFGGTKVEIK 107  
 DB 83 RFSGSGSGTEFTLTISLSQPEDFATYCYCQAHSPFTFGPGTKVDIK 129  
 RESULT 5  
 Q6PIH7 PRELIMINARY; PRT; 236 AA.  
 ID Q6PIH7  
 AC Q6PIH7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC034141; AAH34141.1; -  
 DR HSSP: P01607; 1AR2.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig v.  
 DR Pfam: PF07654; Cl-set; 1.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IGcl; 1.  
 DR SMART: SM00406; IGv; 1.  
 DR PROSITE: PS50835; IG LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;  
 Query Match 85.0%; Score 472; DB 2; Length 236;  
 Best Local Similarity 87.9%; Pred. No. 3.9e-40;  
 Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 DIQWTPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASLSQGVPS 60  
 DB 23 DIQWTPSSVSVASVGRVITTCRASQISVSLAWYQKPKAPKRLIYAASLSQGVPS 82  
 QY 61 RFSGSGSGTEFTLTISLSQPEDFATYCYCLOHNSYPLTFGGTKVEIK 107  
 DB 83 RFSGSGSGTEFTLTISLSQPEDFATYCYCQQLNSPPTFGGTKVEIK 129  
 RESULT 6  
 Q9UL70 PRELIMINARY; PRT; 108 AA.  
 ID Q9UL70  
 AC Q9UL70  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

```
RT fetus." ;
RL Clin. Immunol. Immunopathol. 87:184-192 (1998) .
DR EMBL: AF035044; AAD56280.1; -.
DR PIR: PH0863; PH0863.
DR HSPF: P01607; IHW10.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
Query Match 84.5%; Score 469; DB 2; Length 108;
Best Local Similarity 85.0%; Pred. No. 3.3e-40;
Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGRVTTTCRASQIGIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGRVTTTCRASQIGISNYLAWYQKPKVPSLIYAASLTLSQSGVPS 60
Qy 61 RFSGSGSGTFTLTITSISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTFTLTITSISSLOPEDVATYYCQKNSAPRTFPGGTKLEIK 107
RESULT 7
Q6GMX9 PRELIMINARY; PRT; 236 AA.
ID Q6GMX9
AC Q6GMX9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P.,
RA Raba S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073763; AAH73763.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
```

```
DR Pfam: PF07654; Cl-set; 1.
DR SMART: SM00407; IG; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFE7 CRC64;
Query Match 84.5%; Score 469; DB 2; Length 236;
Best Local Similarity 85.0%; Pred. No. 8e-40;
Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGRVTTTCRASQIGIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 23 DIQWTQSPSSLSASVGRVTTTCRASQVSRNLAWYQORPEKAPKSLIYATSSLSHSGVPS 82
Qy 61 RFSGSGSGTFTLTITSISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 83 RFSGSGSGTFTLTITSISSLOPEDFATYYCQVNTYPLTFGGGTKVEIK 129
RESULT 8
Q65ZC8 PRELIMINARY; PRT; 244 AA.
ID Q65ZC8
AC Q65ZC8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies." ;
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL: Y13057; CAA73500.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; IGV; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17869338F2BF CRC64;
Query Match 84.3%; Score 468; DB 2; Length 244;
Best Local Similarity 83.2%; Pred. No. 1.1e-39;
Matches 89; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGRVTTTCRASQIGIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 137 DIQWTQSPSTLSASTGDRVTTTCRASQIGIYHNLAWYQKPKAPKFLIYKASSLASGAPS 196
Qy 61 RFSGSGSGTFTLTITSISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
Db 197 RFSGSGSGTFTLTITSISSLOPEDFATYYCQVSNYPLTFGGGTKLEIK 243
RESULT 9
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
```



```

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalkska U., Smillutz J., Smillutz D.E., Schnerch A., Schein J.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RC Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 83.1%; Score 461; DB 2; Length 236;
Best Local Similarity 85.0%; Pred.No. 5.3e-39;
Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSLASVGDVRVITTCRASQIGIRNDLIGWYQKFGKAPKRLIYAASSLQGVPS 60
Db 23 DIQWTSPLSLASVGDVRVITTCRASQINNNYQLKPGKAPNLLIYAASSLQGVPS 82

Qy 61 RFGSGSGTEFTLTITSLQPEDFATYCLQHNYSPLTFGGGTVEIK 107
Db 83 RFGSGSGTDFTTITSLRPDDFATYQCQSYNIPLTFGGGTVEIK 129

RESULT 11

```

Q723Y4;  
AC 01-OCT-2003 (TReMBUrel. 25, Created)  
DT DT 01-OCT-2003 (TReMBUrel. 25, Last sequence update)  
DT DT 01-MAR-2004 (TReMBUrel. 26, Last annotation update)  
DE Hypothetical protein.  
DE  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A.  
RP TISSUE=Skeletal Muscle;  
RC MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schen J.E.,

```
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC005332; AA05332.1; -.
DR HSSP; P01834; IHEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7PBF4ED23084BC6 CRC64;

Query Match 83.1%; Score 461; DB 2; Length 236;
Best Local Similarity 84.1%; Pred. No. 5.3e-39;
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 DIQMTQSPSSLSASVGRVTITCRASQDISNYLAWFOQPKAPKSLIYGASSLSQGVQS 82
QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 KFSGSGSGTDFLTITSLQPEDFATYYCQYKSPVTFGGTKLEIK 129

RESULT 12
Q65ZC9 PRELIMINARY; PRT; 240 AA.
ID Q65ZC9
AC Q65ZC9;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC STRAIN=C1G/7;
RX MEDLINE=97362799; PubMed=9219263;
RT "Komtermann R.E., Wing M.G., Winter G.;
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 82.9%; Score 460; DB 2; Length 240;
Best Local Similarity 82.2%; Pred. No. 6.8e-39;
Matches 88; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
|||
```

```
Db 133 DIQMTQSPSTLSASIGDRVTITCRASEGIYRWLAWYQKPKAPKRLIYKASSLSRAP 192
QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
193 RFSGSGSGTDFLTITSLQPEDFATYYCQYKSPVTFGGGTKVEIK 239

RESULT 13
KVIV HUMAN STANDARD; PRT; 108 AA.
ID KVIV HUMAN
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwalet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; K1HUBN.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1
FT DOMAIN 24
FT DOMAIN 35
FT DOMAIN 49
FT DOMAIN 50
FT DOMAIN 56
FT DOMAIN 57
FT DOMAIN 88
FT DOMAIN 97
FT DOMAIN 98
FT DISULFID 23
FT NON_TER 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 82.2%; Score 456; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 7e-39;
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DIQMTQSPSSLSASVGRVTITCRASQSVNYVYAWFOQPKAPKSLIYDASTLSQGVPS 60

QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 NFGSGSGTDFLTITSLQPEDFATYYCQYKSPVTFGGTKVQIK 107

RESULT 14
Q9UL77 PRELIMINARY; PRT; 108 AA.
ID Q9UL77
AC Q9UL77;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match      81.8%; Score 454; DB 2; Length 108;
Best Local Similarity 86.0%; Pred. No. 1.1e-38;
Matches 92; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGINDLGWYQQKPKGKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQISISYLNWYQQKPKGKAPNLLIYAASSLSQSGVPS 60
QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKEIK 107
DB 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQSYSTSWTFEGGTKEIK 107

RESULT 15
KVLS HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01877; KIHWS.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
```

```
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60B45 CRC64;

Query Match      81.4%; Score 452; DB 1; Length 108;
Best Local Similarity 83.2%; Pred. No. 1.8e-38;
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGINDLGWYQQKPKGKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDISHLAWYQQKSGKAPKLLIYASLSLENGVPS 60
QY 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKEIK 107
DB 61 RFSGSGSGTEFTLTISSLQPEDFATYFCQQAHSVPLTFGGGTVDIK 107

Search completed: November 16, 2005, 22:01:51
Job time : 59.9908 secs
```

THIS PAGE BLANK (CEPT)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357A-14  
Perfect score: 555  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLOHNSYPLTFGGTKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	507	91.4	108	2	US-08-378-939-32
2	507	91.4	108	2	US-08-378-939-34
3	502	90.5	107	3	US-09-240-274-29
4	497	89.5	236	1	US-08-157-101A-5
5	489	88.1	108	3	US-09-025-769B-14
6	489	88.1	108	4	US-09-490-070A-14
7	489	88.1	108	4	US-09-490-153-14
8	489	88.1	108	4	US-09-490-324-14
9	481	86.7	107	2	US-07-934-373C-18
10	481	86.7	107	3	US-08-437-642B-18
11	481	86.7	107	4	US-08-146-206C-18
12	481	86.7	107	4	US-09-648-067A-14
13	481	86.7	107	4	US-09-705-686-18
14	481	86.7	107	4	US-09-705-392A-18
15	481	86.7	107	4	US-09-705-398-18
16	481	86.7	107	5	PCT-US93-07832-18
17	481	86.7	108	2	US-08-379-057-29
18	481	86.7	108	3	US-08-974-899-3
19	481	86.7	108	4	US-09-795-798-3
20	478	86.1	108	3	US-08-974-899-2
21	478	86.1	108	4	US-09-795-798-2
22	478	86.1	109	3	US-09-025-769B-28
23	478	86.1	109	3	US-09-025-769B-43
24	478	86.1	109	4	US-09-490-070A-28
25	478	86.1	109	4	US-09-490-070A-43
26	478	86.1	109	4	US-09-490-153-28
27	478	86.1	109	4	US-09-490-153-43

28	478	86.1	109	4	US-09-490-324-28	Sequence 28, Appl
29	478	86.1	109	4	US-09-490-324-43	Sequence 43, Appl
30	477	85.9	107	3	US-08-599-226-1	Sequence 1, Appl
31	477	85.9	107	3	US-09-125-098-1	Sequence 1, Appl
32	477	85.9	107	4	US-09-540-018-1	Sequence 18, Appl
33	477	85.9	108	2	US-08-378-939-18	Sequence 9, Appl
34	476	85.8	107	3	US-08-599-226-9	Sequence 9, Appl
35	476	85.8	107	3	US-09-125-098-9	Sequence 30, Appl
36	476	85.8	107	4	US-09-540-018-9	Sequence 3, Appl
37	476	85.8	236	4	US-07-934-373C-3	Sequence 3, Appl
38	475	85.6	109	2	US-08-437-642B-3	Sequence 3, Appl
39	475	85.6	109	4	US-08-146-206C-3	Sequence 3, Appl
40	475	85.6	109	4	US-09-705-686-3	Sequence 3, Appl
41	475	85.6	109	4	US-09-705-392A-3	Sequence 3, Appl
42	475	85.6	109	4	US-09-705-398-3	Sequence 3, Appl
43	475	85.6	109	5	PCT-US93-07832-3	Sequence 3, Appl
44	475	85.6	109	5	PCT-US93-07832-3	Sequence 18, Appl
45	474	85.4	107	3	US-08-871-488A-18	

ALIGNMENTS

RESULT 1  
US-08-378-939-32  
; Sequence 32, Application US/08378939  
; Patent No. 5876961  
; GENERAL INFORMATION:  
; APPLICANT: CROWE, JAMES SCOTT  
; APPLICANT: LEWIS, ALAN PETER  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH ST. N.W.  
; CITY: WASHINGTON  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,939  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952640  
; FILING DATE: 01-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1808-118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-378-939-32

Query Match 91.4%; Score 507; DB 2; Length 108;  
Best Local Similarity 91.6%; Pred. No. 1.5e-40;  
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLWGYYQOKPGKAPKRLIYAASSLSQGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLWGYYQOKPGKAPKRLIYAASSLSQGVPS 60



```

RESULT 6
US-09-490-070A-14
; Sequence 14, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
;
US-09-490-070A-14

Query Match      88.1%; Score 489; DB 4; Length 108;
Best Local Similarity 90.7%; Pred. No. 7.3e-39;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGINDLGWYQQRPGKAPKRLIYAASSLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQISNYLNWYQKPGKAPKRLIYAASSLQSGVPS 60
QY 61 RFSGSGSGTEFTLTISSLQPEDPATFYCLQHNISYPLTFGGGTKEIK 107
DB 61 RFSGSGSGTDFLTITISLQPEDPATFYCCQYVSTPLTFGGGTKEIK 107

RESULT 7
US-09-490-153-14
; Sequence 14, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming

```

;; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
;; NUMBER OF SEQUENCES: 373  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
;; STREET: 1251 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10021  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/490,153  
;; FILING DATE: 24-Jan-2000  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/025,769B  
;; FILING DATE: 18-FEB-1998  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 108 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-490-153-14  
  
Query Match 88.1%; Score 489; DB 4; Length 108;  
Best Local Similarity 90.7%; Pred. No. 7.3e-39;  
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKGKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIYNLWYQKPKGKAPKRLIYAASSLSQSGVPS 60  
  
Qy 61 RFGSGSGTFTLTITSSLPQEDPATYICLOHNSYPLTFGGGTKVEIK 107  
Db 61 RFGSGSGTFTLTITSSLPQEDPATYICQYYSYPLTFGGGTKVEIK 107  
  
RESULT 8  
US-09-490-324-14  
; Sequence 14, Application US/09490324  
; Patent No. 6828422  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/490,324  
;; FILING DATE: 24-Jan-2000  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/025,769  
;; FILING DATE: 18-FEB-1998  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 108 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-490-324-14  
  
Query Match 88.1%; Score 489; DB 4; Length 108;  
Best Local Similarity 90.7%; Pred. No. 7.3e-39;  
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKGKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIYNLWYQKPKGKAPKRLIYAASSLSQSGVPS 60  
  
Qy 61 RFGSGSGTFTLTITSSLPQEDPATYICLOHNSYPLTFGGGTKVEIK 107  
Db 61 RFGSGSGTFTLTITSSLPQEDPATYICQYYSYPLTFGGGTKVEIK 107  
  
RESULT 9  
US-07-934-373C-18  
; Sequence 18, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991



```
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-07-934-373C-18
Query Match 86.7%; Score 481; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQSIKNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFGSGSGTFTLTITSSLPQEDPATYICLOHNSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPQEDPATYICQYNSLPWTFGGTKVEIK 107

RESULT 10
US-08-437-642B-18
; Sequence 18, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-437-642B-18
Query Match 86.7%; Score 481; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQSIKNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFGSGSGTFTLTITSSLPQEDPATYICLOHNSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPQEDPATYICQYNSLPWTFGGTKVEIK 107

RESULT 11
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-146-206C-18
Query Match 86.7%; Score 481; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQSIKNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFGSGSGTFTLTITSSLPQEDPATYICLOHNSYPLTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPQEDPATYICQYNSLPWTFGGTKVEIK 107
```

```

RESULT 12
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: PI775R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-27
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14

Query Match      86.7%; Score 481; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITTCRASQGIKNDLQWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITTCRASQSIISNYLAWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFSGSGSGTFTLTITSSLPQDFATYYCQYNSLPFTFGGQTKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLPQDFATYYCQYNSLPFTFGGQTKVEIK 107

RESULT 13
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-Nov. 6639055-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994

```

```

; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match      86.7%; Score 481; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITTCRASQGIKNDLQWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITTCRASQSIISNYLAWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFSGSGSGTFTLTITSSLPQDFATYYCQYNSLPFTFGGQTKVEIK 107
Db 61 RFSGSGSGTFTLTITSSLPQDFATYYCQYNSLPFTFGGQTKVEIK 107

RESULT 14
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,392A
; FILING DATE: 02-Nov. 6719971-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18

Query Match      86.7%; Score 481; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.1e-38;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITTCRASQGIKNDLQWYQKPKGKAPKRLIYAASSLSQSGVPS 60

```

Db 1 DIQWTQSPSSLSASVGRVITTCRASQSIGNSYLAWYQQKFGKAPKRLIYAASSLESQVPS 60  
Qy 61 RFGSGSGTFTLTITSSLPEDFATYYCLOHNSYPLTFGGGTKVEIK 107  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 61 RFGSGSGTFTLTITSSLPEDFATYYCQYNSLPTWTFGGGTKVEIK 107

RESULT 15  
US-09-705-398-18  
; Sequence 18, Application US/09705398  
; Patent No. 6800738  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/705,398  
; FILING DATE: 02-Nov-6800738-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P1D2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-705-398-18

Query Match 86.7%; Score 481; DB 4; Length 107;  
Best Local Similarity 88.8%; Pred. No. 4.1e-38;  
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 DIQWTQSPSSLSASVGRVITTCRASQIGIRNDLQWYQQKFGKAPKRLIYAASSLSQVPS 60  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 1 DIQWTQSPSSLSASVGRVITTCRASQISYLAWYQQKFGKAPKRLIYAASSLESQVPS 60  
Qy 61 RFGSGSGTFTLTITSSLPEDFATYYCLOHNSYPLTFGGGTKVEIK 107  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 61 RFGSGSGTFTLTITSSLPEDFATYYCQYNSLPTWTFGGGTKVEIK 107

Search completed: November 16, 2005, 22:07:19  
Job time : 19.1939 secs

THIS PAGE BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds  
(without alignments)  
681.481 Million cell updates/sec

Title: US-10-660-357A-14  
Perfect score: 555  
Sequence: 1 DIQMTSPSLASVGDVRT.....CLQHNSYPLTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	100.0	107	14	US-10-330-613-14
2	555	100.0	107	14	US-10-330-530-14
3	555	100.0	107	14	US-10-041-860-18
4	555	100.0	107	14	US-10-041-860-233
5	555	100.0	107	14	US-10-041-860-267
6	555	100.0	107	14	US-10-041-860-285
7	555	100.0	107	15	US-10-309-762-51
8	555	100.0	107	16	US-10-660-357-14
9	555	100.0	107	16	US-10-665-383-16
10	555	100.0	107	17	US-10-727-155-208
11	555	100.0	107	17	US-10-727-155-220
12	555	100.0	107	14	Sequence 14, Appl
13	555	100.0	107	14	Sequence 14, Appl
14	555	100.0	107	14	Sequence 18, Appl
15	555	100.0	107	14	Sequence 233, Appl
16	555	100.0	107	14	Sequence 267, Appl
17	555	100.0	107	14	Sequence 285, Appl
18	555	100.0	107	15	Sequence 51, Appl
19	555	100.0	107	16	Sequence 14, Appl
20	555	100.0	107	16	Sequence 16, Appl
21	555	100.0	107	17	Sequence 208, Appl
22	555	100.0	107	17	Sequence 220, Appl

12	555	100.0	107	17	US-10-727-155-273	Sequence 273, App
13	555	100.0	107	17	US-10-727-155-305	Sequence 305, App
14	555	100.0	107	17	US-10-877-773-24	Sequence 24, Appl
15	555	100.0	107	17	US-10-877-774-24	Sequence 24, Appl
16	555	100.0	108	17	US-10-805-177-62	Sequence 62, Appl
17	554	99.8	108	17	US-10-805-177-4	Sequence 4, Appl
18	554	99.8	168	17	US-10-805-177-115	Sequence 115, App
19	552	99.5	107	17	US-10-727-155-4	Sequence 4, Appl
20	552	99.5	107	17	US-10-727-155-28	Sequence 28, Appl
21	551	99.3	107	14	US-10-041-860-14	Sequence 14, Appl
22	551	99.3	107	14	US-10-041-860-229	Sequence 229, App
23	551	99.3	107	14	US-10-041-860-263	Sequence 263, App
24	551	99.3	107	16	US-10-665-383-8	Sequence 8, Appl
25	551	99.3	107	17	US-10-727-155-224	Sequence 224, App
26	551	99.3	107	17	US-10-893-576-176	Sequence 176, App
27	551	99.3	129	17	US-10-893-576-40	Sequence 40, Appl
28	548	98.7	107	15	US-10-309-762-57	Sequence 57, Appl
29	548	98.7	107	17	US-10-727-155-8	Sequence 8, Appl
30	547	98.6	153	15	US-10-309-762-245	Sequence 245, App
31	546	98.4	107	17	US-10-727-155-12	Sequence 12, Appl
32	546	98.4	107	17	US-10-727-155-32	Sequence 32, Appl
33	546	98.4	107	17	US-10-727-155-126	Sequence 126, App
34	546	98.4	107	17	US-10-893-576-175	Sequence 175, App
35	546	98.4	129	17	US-10-893-576-34	Sequence 34, Appl
36	544	98.0	107	15	US-10-309-762-58	Sequence 58, Appl
37	544	98.0	107	16	US-10-684-109-57	Sequence 57, Appl
38	543	97.8	234	16	US-10-684-109-115	Sequence 115, App
39	543	97.8	107	17	US-10-727-155-256	Sequence 256, App
40	543	97.8	110	16	US-10-312-316-52	Sequence 52, Appl
41	542	97.7	107	17	US-10-727-155-40	Sequence 40, Appl
42	542	97.7	107	17	US-10-727-155-44	Sequence 44, Appl
43	542	97.7	107	17	US-10-727-155-78	Sequence 78, Appl
44	541	97.5	107	17	US-10-727-155-252	Sequence 252, App
45	541	97.5	107	14	US-10-330-613-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-14  
; Sequence 14, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-14

Query Match 100.0%; Score 555; DB 14; Length 107;  
Best Local Similarity 100.0%; Pred. No. 99-40;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DIQMTSPSLASVGDVRTITCRASQGI	RNDLGTWYQKPKAPKRLIYAASSLSQGVPS	60
Db	1	DIQMTSPSLASVGDVRTITCRASQGI	RNDLGTWYQKPKAPKRLIYAASSLSQGVPS	60
Qy	61	RFGSGSGTEFTLTISLQPEDPATYVC	LOHNSYPLTFGGTKVEIK	107
Db	61	RFGSGSGTEFTLTISLQPEDPATYVC	LOHNSYPLTFGGTKVEIK	107

RESULT 2

```
US-10-330-530-14
; Sequence 14, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Cudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-330-530-14

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107

RESULT 3
US-10-041-860-18
; Sequence 18, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-18

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107

RESULT 4
US-10-041-860-233
; Sequence 233, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-233

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107

RESULT 5
US-10-041-860-267
; Sequence 267, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-267

Query Match 100.0%; Score 555; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPLTFGGGTKVEIK 107
```

Db 61 RFGSGSGTEFTLTITSSLOPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

## RESULT 6

US-10-041-860-285  
; Sequence 285, Application US/10041860  
; Publication No. US20030157109A1

## GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadi

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: AGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041.860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 285

; LENGTH: 107

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-285

Query Match 100.0%; Score 555; DB 14; Length 107;

Best Local Similarity 100.0%; Pred. No. 9e-40;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVSGDRVTITCRASQIRNDLWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQWTSPLSASVSGDRVTITCRASQIRNDLWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLOPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

Db 61 RFGSGSGTEFTLTITSSLOPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

## RESULT 7

US-10-309-762-51

; Sequence 51, Application US/10309762

; Publication No. US20040018198A1

## GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; APPLICANT: Foltz, Ian

; APPLICANT: Handa, Masahisa

; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; FILE REFERENCE: AGENIX.027A

; CURRENT APPLICATION NUMBER: US/10/309.762

; CURRENT FILING DATE: 2002-12-02

; PRIOR APPLICATION NUMBER: 60/337275

; PRIOR FILING DATE: 2001-12-03

; NUMBER OF SEQ ID NOS: 245

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 51

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-309-762-51

Query Match 100.0%; Score 555; DB 15; Length 107;

Best Local Similarity 100.0%; Pred. No. 9e-40;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVSGDRVTITCRASQIRNDLWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQWTSPLSASVSGDRVTITCRASQIRNDLWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLOPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

Db 61 RFGSGSGTEFTLTITSSLOPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

## RESULT 8

US-10-660-357-14

; Sequence 14, Application US/10660357

; Publication No. US20040115205A1

## GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe

; APPLICANT: Green, Larry L.

; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

; TITLE OF INVENTION: ANTIGEN

; FILE REFERENCE: AGENIX.030C1

; CURRENT APPLICATION NUMBER: US/10/660.357

; CURRENT FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 10/330.580

; PRIOR FILING DATE: 2002-12-26

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-660-357-14

Query Match 100.0%; Score 555; DB 16; Length 107;

Best Local Similarity 100.0%; Pred. No. 9e-40;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVSGDRVTITCRASQIRNDLWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQWTSPLSASVSGDRVTITCRASQIRNDLWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLOPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

Db 61 RFGSGSGTEFTLTITSSLOPEDPATYCYCLOHNSYPLTFGGTKVEIK 107

## RESULT 9

US-10-665-383-16

; Sequence 16, Application US/10665383

; Publication No. US20040141969A1

## GENERAL INFORMATION:

; APPLICANT: Floege, Juergen

; APPLICANT: Gazit, Gadi

; APPLICANT: Keyt, Bruce

; APPLICANT: LaRochele, William

; APPLICANT: Lichenstein, Henri

; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS

; FILE REFERENCE: AGENIX.052A

; CURRENT APPLICATION NUMBER: US/10/665.383

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: 60/411.137

; PRIOR FILING DATE: 2002-09-16

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 107

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-665-383-16

Query Match 100.0%; Score 555; DB 16; Length 107;

Best Local Similarity 100.0%; Pred. No. 9e-40;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVSGDRVTITCRASQIRNDLWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 1 DIQWTSPLSASVSGDRVTITCRASQIRNDLWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFSGSGTETLTIISSLPEDFATYYCLOHNSYPLTFGGGTVKEIK 107  
|||  
Db 61 RFSGSGTETLTIISSLPEDFATYYCLOHNSYPLTFGGGTVKEIK 107

RESULT 10  
US-10-727-155-208  
; Sequence 208, Application US/10727155  
; Publication No. US20050049402A1

Query Match 100.0%; Score 555; DB 17; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-40;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 RFSGSGTETLTIISSLPEDPATYYCLOHNSYPLTFGGGTKEIK 107  
|||

Db 61 RFSGSGTETLTIISSLPEDPATYYCLOHNSYPLTFGGGTKEIK 107

RESULT 11  
US-10-727-155-220  
; Sequence 220, Application US/10727155  
; Publication No. US20050049402A1

; APPLICANT: QIAOJUAN JANE SU  
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
 ; TITLE OF INVENTION: FACTOR AND USES THEREOF  
 ; FILE REFERENCE: A8ENTX.073A

```
Query Match      100.0%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 61 RFSGSGGTETLTIISSLPEDFATYYCLOHNSYPLTFGGGKVEIK 107  
 |||||  
 61 RFSGSGGTETLTIISSLPEDFATYYCLOHNSYPLTFGGGKVEIK 107

pb 61 RFSGSGGTETLTIISSLPEDFATYYCLOHNSYPLTFGGGKVEIK 107  
 |||||

RESULT 12  
US-10-727-155-273  
; Sequence 273, Application US/10727155  
; Publication No. US20050049402A1

Query Match 100.0%; Score 555; DB 17; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-40;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

61 RFSGSGGTEFTLTITSSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107



Db 61 RFSGSGGTEFTLTIISSLOPEDFATYTCLOHNSYPLTFGGGTKEIK 107

RESULT 13

US-727-155-305  
; Sequence 305, Application US/10727155  
; Publication No. US20050049402A1  
GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaespal S. Kang  
; APPLICANT: Orit Poord  
; APPLICANT: Larry Green  
; APPLICANT: Xiao Feng  
; APPLICANT: Scott Klakamp  
; APPLICANT: Mary Haak-Frendtscho  
; APPLICANT: Palaniswami Rathanswami  
; APPLICANT: Craig Pigott  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Manchulenko  
; APPLICANT: Raffaella Paggioni  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Qiaotuan Jane Su

	Query Match	100.0%;	Score 555;	DB 17;	Length 107;
	Best Local Similarity	100.0%;	Prod. No. 9e-40;		
	Matches 107;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	DIQWQTSPSLSASVGRVVTITCRASQGI	RNDLGWYQOKPKAPRLIYAASSLQSGVPS	60	
Db	1	DIQWQTSPSLSASVGRVVTITCRASQGI	RNDLGWYQOKPKAPRLIYAASSLQSGVPS	60	
Qy	61	RFGSGSGTFTLTITSSLSQPEDFATYCY	LOHNSYPLTFGGGKTVEIK	107	
Db	61	RFGSGSGTFTLTITSSLSQPEDFATYCY	LOHNSYPLTFGGGKTVEIK	107	

RESIT.T 14

```

RESULI 14
US-10-877-773-24
; Sequence 24, Application US/10877773
; Publication No. US20050053608A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Richard
; APPLICANT: Feng, Xiao
; APPLICANT: Foord, Ortt
; APPLICANT: Green, Larry
; APPLICANT: Gudas, Jean
; APPLICANT: Keyat, Bruce
; APPLICANT: Liu, Ying
; APPLICANT: Rathnaswami, Palani
; APPLICANT: Rava, Robert
; APPLICANT: Yang, Xiao Dong
; APPLICANT: Corvalan, Jose
; APPLICANT: Foltz, Ian
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Kang, Jaspal
; APPLICANT: King, Chadwick T.
; APPLICANT: Klamang, Scott L.

```

```

; APPLICANT: Su, Qiaojuan Jane
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
; OF INVENTION: MUTANTS OF EPIDERMAL GROWTH FACTOR RECEPTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.087A
; CURRENT APPLICATION NUMBER: US/10/877,773
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: 60/483,145
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/525,570
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/562,453
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 107
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-877-773-24

```

	Query Match	100.0%;	Score 555;	DB 17;	Length 107;
	Best Local Similarity	100.0%;	Pred. No. 9e-40;		
	Matches 107;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	DIQWTQPSLSASVGRVTTITCRASQIRINDLGWYQKPKGAPKRLIYAASSLSQGVPS	60		
Db	1	DIQWTQPSLSASVGRVTTITCRASQIRINDLGWYQKPKGAPKRLIYAASSLSQGVPS	60		
Qy	61	RFGSGSGTEFTTITISLQPEDPATYCYLOHNSYPLTFGGGTQVKEIK	107		
Db	61	RFGSGSGTEFTTITISLQPEDPATYCYLOHNSYPLTFGGGTQVKEIK	107		

## RESULT 15

```

US-10-877-774-24
; Sequence 24, Application US/10877774
; Publication No. US20050987A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Weber, Richard
; APPLICANT: Feng, Xiao
; APPLICANT: Food, Orly
; APPLICANT: Green, Larry
; APPLICANT: Gudas, Jean
; APPLICANT: Kevt, Bruce
; APPLICANT: Liu, Ying
; APPLICANT: Rathanaswami, Palani
; APPLICANT: Raya, Robert
; APPLICANT: Yang, Xiao Dong
; APPLICANT: Corvalan, Jose
; APPLICANT: Foltz, Ian
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Kang, Jaspal
; APPLICANT: King, Chadwick T.
; APPLICANT: Klakamp, Scott L.
; APPLICANT: Su, Qiaojuan Jane
;
; TITLE OF INVENTION: ANTIBODIES DIRE
; TITLE OF INVENTION: MUTANTS OF EPI
; FILE REFERENCE: AGENIX.087A2
; CURRENT APPLICATION NUMBER: US/10/8
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: 60/483,14
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/525,57
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/562,45
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Versi
; SEQ ID NO 24
;
; LENGTH: 107
; TYPE: PRP
;
; ORGANISM: Homo sapiens
; US-10-877-774-24

```

```

Query Match      100.0%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTTITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLQSGVPS 60
   |||||||
Db 1 DIQMTQSPSSLSASVGDRTTITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLQSGVPS 60
   |||||||

Qy 61 RFSGSGGTFTLTISSLQPEDFATYVCLQHNSEYPLTFGGGTKVEIK 107
   |||||||
Db 61 RFSGSGGTFTLTISSLQPEDFATYVCLQHNSEYPLTFGGGTKVEIK 107
   |||||||

```

Search completed: November 16, 2005, 23:05:41  
 Job time : 66.6949 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-18

Perfect score: 561

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLOHNSYPWTFGGTKVRIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561	100.0	107	7	Adc99789 Anti-huma
2	561	100.0	107	7	Adc99789 Anti-MUC1
3	561	100.0	107	7	Adf05393 Anti-MUC1
4	561	100.0	107	7	Adf09831 Human ant
5	561	100.0	107	7	Adk18842 Anti-huma
6	561	100.0	107	7	Adk18916 Anti-huma
7	561	100.0	107	7	Adk18892 Anti-huma
8	561	100.0	107	7	Adk18612 Anti-huma
9	561	100.0	107	7	Adk18602 Anti-huma
10	561	100.0	107	7	Adk18810 Anti-huma
11	561	100.0	107	7	Adk18844 Anti-huma
12	561	100.0	107	7	Adk18808 Anti-huma
13	561	100.0	107	7	Adk18807 Anti-huma
14	561	100.0	107	7	Adk18604 Anti-huma
15	561	100.0	107	8	Adp03996 Murine-ex
16	561	100.0	107	8	Adl25422 Human mab
17	561	100.0	107	8	Adl25426 Human mab
18	561	100.0	107	8	Ado07289 Human pro
19	561	100.0	107	8	Adp22368 Human ant
20	561	100.0	107	8	Adp22401 Human ant
21	561	100.0	236	5	Abg77164 Germline
22	561	100.0	236	8	Adr28586 Human ant
23	558	99.5	107	7	Adk18841 Anti-huma
24	556	99.1	107	8	Adp22158 Human ant
25	551	98.2	107	7	Adk18885 Anti-huma

26	549	97.9	107	8	ADP22110 Human ant
27	549	97.9	107	8	ADP22354 Human ant
28	549	97.9	236	5	ABG77160 Germline
29	549	97.9	236	8	ADR28582 Human ant
30	548	97.7	107	7	ADK18840 Anti-huma
31	548	97.7	107	7	ADK18879 Anti-huma
32	548	97.7	107	7	ADK18806 Anti-huma
33	548	97.7	107	7	ADK18600 Anti-huma
34	548	97.7	107	8	ADL25418 Human mab
35	548	97.7	236	8	ADP07905 Human imm
36	547	97.5	107	8	ADP22154 Human ant
37	546	97.3	108	8	ADP47296 Human pho
38	545	97.1	107	7	ADP03916 Murine-ex
39	545	97.1	107	7	ADP03912 Murine-ex
40	545	97.1	107	7	ADP03908 Murine-ex
41	545	97.1	107	7	ADP03913 Murine-ex
42	542	96.6	152	8	ADK52390 Human ant
43	541	96.4	107	7	ADC99785 Anti-huma
44	541	96.4	107	7	ADD05389 Anti-MUC1
45	541	96.4	107	7	ADF09827 Human ant

## ALIGNMENTS

RESULT 1  
ADC99789

ID ADC99789 standard; protein; 107 AA.

XX ADC99789;

DT 01-JAN-2004 (first entry)

XX Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 18.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.

OS Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

DR N-PSDB; ADC99791.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

XX Claim 3; SEQ ID NO 18; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

CC light chain protein of the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 561; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTFTLTITISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107  
Db 61 RFGSGSGTFTLTITISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 2

ADD05393  
ID ADD05393 standard; protein; 107 AA.  
XX  
AC ADD05393;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID NO 18.  
XX  
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057006-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041582.  
XX  
PR 28-DEC-2001; 2001US-0346460P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J, Bar-Eli M;  
XX  
XX WPI; 2003-577496/54.  
DR N-PSDB; ADD05395.  
XX

Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumor.

Claim 3; SEQ ID NO 18; 87pp; English.

The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region, protein of the invention.

Sequence 107 AA;

Query Match 100.0%; Score 561; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTFTLTITISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107  
Db 61 RFGSGSGTFTLTITISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 3

ADF09831  
ID ADF09831 standard; protein; 107 AA.  
XX  
AC ADF09831;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human anti-MUC18 monoclonal antibody light chain #5.  
XX  
KW cell proliferation inhibition; MUC18 tumour antigen;  
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
KW carcinoma; cancer; malignancy; light chain; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057837-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041580.  
XX  
PR 28-DEC-2001; 2001US-0346414P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
XX WPI; 2003-598367/56.  
DR N-PSDB; ADF09833.  
XX

Inhibiting cell proliferation associated with expression of MUC18 tumour antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.

Claim 3; SEQ ID NO 18; 83pp; English.

The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific monoclonal antibody.

Sequence 107 AA;

Query Match 100.0%; Score 561; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTFTLTITISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107  
Db 61 RFGSGSGTFTLTITISSLPQEDFATYYCLOHNSYPWTFGGQTKVEIK 107

```

RESULT 4
ADK18916
ID ADK18916 standard; protein; 107 AA.
XX AC ADK18916;
XX DT DT (first entry)
XX DE Anti-human PDGF-D antibody related sequence #68.
DE antiinflammatory; immunomodulator; cytostatic; gene therapy.
KW Homo sapiens.
XX OS WO2003057857-A2.
XX XX 17-JUL-2003.
XX XX 06-JAN-2003; 2003WO-US000398.
XX PF 07-JAN-2002; 2002US-00041860.
PR ABGE-) ABGENIX INC.
XX PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R; Bezabeh B;
XX DR WPI; 2003-587119/55.
XX PT New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
XX PP Disclosure; SEQ ID NO 266; 255pp; English.
XX CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCDP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 561; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMOTSPSLASVGRDVTITCRASGIRNDLGWYOQKPKAPRLIYAASSLSQGVS 60
DB 1 DIQMOTSPSLASVGRDVTITCRASGIRNDLGWYOQKPKAPRLIYAASSLSQGVS 60
QY 61 RFSGSGGTFTLTIISSLPEDFATYYCLOHNSYPWTFGQTKEIK 107
DB 61 RFSGSGGTFTLTIISSLPEDFATYYCLOHNSYPWTFGQTKEIK 107
RESULTS
ADK18916
ID ADK18916 standard; protein; 107 AA.
XX AC ADK18916;
XX DT DT (first entry)
XX DE Anti-human PDGF-D antibody related sequence #142.
XX PP
```

PA (ABGE-) ABGENIX INC.  
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX WPI; 2003-587119/55.  
XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX Disclosure; SEQ ID NO 316; 255pp; English.  
XX  
CC The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX  
XX Sequence 107 AA;  
XX  
Query Match 100.0%; Score 561; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPWTFGGTKVEIK 107  
Db 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPWTFGGTKVEIK 107  
RESULT 7  
ADK18612  
ID ADK18612 standard; protein; 107 AA.  
XX  
AC ADK18612;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Anti-human PDGF-D antibody light chain protein sequence.  
XX  
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO2003057857-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 06-JAN-2003; 2003WO-US000398.  
XX  
PR 06-JAN-2003; 2003WO-US000398.  
XX  
PS 07-JAN-2002; 2002US-00041860.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX  
DR WPI; 2003-587119/55.  
XX  
XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX Disclosure; SEQ ID NO 36; 255pp; English.  
XX

XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX  
XX Sequence 107 AA;  
XX  
Query Match 100.0%; Score 561; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPWTFGGTKVEIK 107  
Db 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSYPWTFGGTKVEIK 107  
RESULT 8  
ADK18602  
ID ADK18602 standard; protein; 107 AA.  
XX  
AC ADK18602;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Anti-human PDGF-D antibody light chain protein sequence.  
XX  
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO2003057857-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 06-JAN-2003; 2003WO-US000398.  
XX  
PR 07-JAN-2002; 2002US-00041860.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX  
DR WPI; 2003-587119/55.  
XX  
PT New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX Disclosure; SEQ ID NO 26; 255pp; English.  
XX  
XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX

SQ Sequence 107 AA;  
Query Match 100.0%; Score 561; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGRVTITCRASQIRNDLWYQKPGKAPKRLIYAASSLSQGVPS 60  
DB 1 DIQWTSPLSASVGRVTITCRASQIRNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

QY 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107  
DB 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107

RESULT 9  
ADK18810  
ID ADK18810 standard; protein; 107 AA.  
AC ADK18810;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Anti-human PDGF-D antibody protein related sequence #36.  
XX  
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX WO2003057857-A2.  
XX  
XX 17-JUL-2003.  
XX  
XX 06-JAN-2003; 2003WO-US000398.  
XX  
XX 07-JAN-2002; 2002US-00041860.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;  
XX  
XX WPI; 2003-587119/55.  
XX  
XX New human monoclonal antibody that binds to platelet-derived growth  
XX factor-D (PDGF-D), useful for treating chronic and recurrent human  
XX diseases, such as inflammation, autoimmunity and cancer.  
XX  
XX Disclosure; SEQ ID NO 234; 255pp; English.

CC The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.

SQ Sequence 107 AA;  
Query Match 100.0%; Score 561; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGRVTITCRASQIRNDLWYQKPGKAPKRLIYAASSLSQGVPS 60  
DB 1 DIQWTSPLSASVGRVTITCRASQIRNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

QY 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107  
DB 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107

RESULT 11  
ADK18808  
ID ADK18808 standard; protein; 107 AA.  
XX  
XX ADK18808;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Anti-human PDGF-D antibody protein related sequence #34.

DB 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107

RESULT 10  
ADK18844  
ID ADK18844 standard; protein; 107 AA.  
XX  
XX ADK18844;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Anti-human PDGF-D antibody protein related sequence #70.  
XX  
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX WO2003057857-A2.  
XX  
XX 17-JUL-2003.  
XX  
XX 06-JAN-2003; 2003WO-US000398.  
XX  
XX 07-JAN-2002; 2002US-00041860.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;  
XX  
XX WPI; 2003-587119/55.  
XX  
XX New human monoclonal antibody that binds to platelet-derived growth  
XX factor-D (PDGF-D), useful for treating chronic and recurrent human  
XX diseases, such as inflammation, autoimmunity and cancer.  
XX  
XX Disclosure; SEQ ID NO 268; 255pp; English.

CC The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.

SQ Sequence 107 AA;  
Query Match 100.0%; Score 561; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTSPLSASVGRVTITCRASQIRNDLWYQKPGKAPKRLIYAASSLSQGVPS 60  
DB 1 DIQWTSPLSASVGRVTITCRASQIRNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

QY 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107  
DB 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107

RESULT 11  
ADK18808  
ID ADK18808 standard; protein; 107 AA.  
XX  
XX ADK18808;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Anti-human PDGF-D antibody protein related sequence #34.

XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX Homo sapiens.  
 OS WO2003057857-A2.  
 PN 17-JUL-2003.  
 PD 06-JAN-2003; 2003WO-US000398.  
 XX 07-JAN-2002; 2002US-00041860.  
 PR (ABGE-) ABGENIX INC.  
 PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 DR WPI; 2003-587119/55.  
 XX New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 XX Disclosure; SEQ ID NO 232; 255pp; English.  
 PS The invention relates to a human monoclonal antibody that binds to  
 XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.  
 XX Sequence 107 AA;  
 SQ

Query Match 100.0%; Score 561; DB 7; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGYQQKPKAPKRLIYAASSLSQGVPS 60  
 Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGYQQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLPEDFATYYCLOHNSYPWTFGGTKVEIK 107  
 Db 61 RFGSGSGTEFTLTITSSLPEDFATYYCLOHNSYPWTFGGTKVEIK 107

RESULT 12  
 ADK18807  
 ID ADK18807 standard; protein; 107 AA.  
 AC ADK18807;  
 XX 06-MAY-2004 (first entry)  
 DT Anti-human PDGF-D antibody protein related sequence #33.  
 DE antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 KW Homo sapiens.  
 OS WO2003057857-A2.  
 PN 17-JUL-2003.  
 PD 06-JAN-2003; 2003WO-US000398.  
 XX 07-JAN-2002; 2002US-00041860.  
 PR

XX (ABGE-) ABGENIX INC.  
 XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX WPI; 2003-587119/55.  
 XX New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 XX Disclosure; SEQ ID NO 231; 255pp; English.  
 PS The invention relates to a human monoclonal antibody that binds to  
 XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.  
 XX Sequence 107 AA;  
 SQ

Query Match 100.0%; Score 561; DB 7; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGYQQKPKAPKRLIYAASSLSQGVPS 60  
 Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLGYQQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLPEDFATYYCLOHNSYPWTFGGTKVEIK 107  
 Db 61 RFGSGSGTEFTLTITSSLPEDFATYYCLOHNSYPWTFGGTKVEIK 107

RESULT 13  
 ADK18604  
 ID ADK18604 standard; protein; 107 AA.  
 AC ADK18604;  
 XX 06-MAY-2004 (first entry)  
 DT Anti-human PDGF-D antibody light chain protein sequence.  
 DE antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 KW Homo sapiens.  
 OS WO2003057857-A2.  
 PN 17-JUL-2003.  
 PD 06-JAN-2003; 2003WO-US000398.  
 XX 07-JAN-2002; 2002US-00041860.  
 PR (ABGE-) ABGENIX INC.  
 PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX WPI; 2003-587119/55.  
 XX New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 XX



The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renalcell carcinoma, cervixcarcinoma,

CC monoclonal antibody (mAb) variable region sequence, which is used in the  
CC exemplification of the present invention.

Түркістан аймағындағы қызыл және қызыл-сары топырақтардың құрамы мен құрылымы

33

Sequence 107 AA;

```
Query Match      100.0%; Score 561; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Query Match	100.0%;	Score 561;	DB 8;
Best Local Similarity	100.0%;	Pred. No. 5.9e-35;	

Best local similarity 100.00%, Rec. NO. 3.58-35,  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCRASQGI RNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60

Db

1 DIQMTQSPSSLASVGDRTITCRASQGIKNDLGWYQKPKGKAPKRLIYAASSLQSGVPS 60

Qy 61 RFSGSGTGTEFTLTISSLPQPEDFATYYCLQNSYPWTFGQTKVEIK 107

Db 61 RFSGSGGTEFTLTIISSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107

Search completed: November 16, 2005, 21:51:38

SEARCH COMPLETED: NOVEMBER 1976  
Job time : 61.3676 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-18

Perfect score: 561

Sequence: 1 DIQMTSPSSLSASVGRVT.....CLQHSYPWTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	93.2	125	S40353	Ig kappa chain V-J
2	521	92.9	108	K1HUWE	Ig kappa chain V-I
3	511	91.1	123	S40313	Ig kappa chain V-J
4	510	90.9	108	K1HUGL	Ig kappa chain V-I
5	495	88.2	125	S40333	Ig kappa chain V-J
6	494	88.1	117	S41809	Ig kappa chain V
7	489	87.2	107	S36269	Ig lambda chain V
8	488	87.0	107	S36262	Ig lambda chain V
9	485	86.5	127	S40367	Ig kappa chain V-J
10	485	86.5	129	S40369	Ig kappa chain - h
11	481.5	85.8	124	S40336	Ig kappa chain V-J
12	480	85.6	126	S40335	Ig kappa chain V-J
13	479	85.4	108	S36279	Ig lambda chain V
14	473	84.3	123	S40331	Ig kappa chain - h
15	473	84.3	132	S40334	Ig kappa chain - h
16	472	84.1	132	S46377	Ig kappa chain V-J
17	470	83.8	125	S40349	Ig kappa chain V-J
18	469	83.6	131	S40352	Ig kappa chain V-J
19	467	83.2	95	S69898	Ig kappa chain V
20	467	83.2	108	B49047	Ig kappa chain V
21	467	83.2	141	R49134	Ig kappa chain V-I
22	466	83.1	108	K1HUSE	Ig kappa chain V-I
23	464	82.7	117	S46371	Ig kappa chain V-J
24	463	82.5	107	T69017	anti-HIV1 envelope
25	463	82.5	124	S40318	Ig kappa chain V
26	462	82.4	107	S36264	Ig lambda chain V
27	462	82.4	108	S44122	Ig kappa chain V
28	461	82.2	108	S19674	Ig kappa chain V
29	460.5	82.1	107	S36275	Ig lambda chain V

ALIGNMENTS

RESULT 1

S40353

Ig kappa chain V-J-C region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C;Accession: S40353

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40353

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-125 <KLE>

A;Cross-references: EMBL:X72463

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;30-104/Domain: immunoglobulin homology <IMW>

Query Match 93.2% Score 523; DB 2; Length 125;

Best Local Similarity 94.4%; Pred. No. 2.1e-37;

Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGRVTITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 60

Db 15 DIQMTSPSSLSASVGRVTITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 74

Qy 61 RFGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107

Db 75 RFGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 121

RESULT 2

K1HUWE

Ig kappa chain V-I region (WEA) - human

C;Species: Homo sapiens (man)

C;Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004

C;Accession: A01876

R;Goni, F.; Frangione, B.

Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983

A;Title: Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) wit

A;Reference number: A93964; MUID:83273707; PMID:6410398

A;Accession: A01876

A;Molecule type: protein

A;Residues: 1-108 <GON>

A;Cross-references: UNIPROT:P01610

C;Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated gal

C;Genetics:

A;Gene: GDB:IGKV1

A;Cross-references: GDB:136264

A;Map position: 2p12-2p12

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp

hain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status predicted

Query Match 92.9%; Score 521; DB 1; Length 108;  
Best Local Similarity 91.6%; Pred. No. 2.7e-37;  
Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 DIQWTPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQWTPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTFTLTITSSLOPEDFATYCYCLOHNSYPWTFGQGTKEIK 107  
Db 61 RFGSGSGTFTLTITSSLOPEDFATYCYCLOHNSYPWTFGQGTKEIK 107

RESULT 3  
S40313  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40313  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40313  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-123 <KLE>  
A:Cross-references: EMBL:X72423; NID:g441314; PIDN:CAA51091.1; PID:g441315  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 91.1%; Score 511; DB 2; Length 123;  
Best Local Similarity 92.5%; Pred. No. 2.1e-36;  
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 DIQWTPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 17 DIQWTPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQSGVPS 76  
Qy 61 RFGSGSGTFTLTITSSLOPEDFATYCYCLOHNSYPWTFGQGTKEIK 107  
Db 77 RFGSGSGTFTLTITSSLOPEDFATYCYCLOHNSYPWTFGQGTKEIK 123

RESULT 4  
KIHUGL  
Ig kappa chain V-I region (Gal) - human (tentative sequence)  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C:Accession: A01867  
R:Laure, C.J.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973  
A:Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I  
A:Reference number: A01867; MUID:75059122; PMID:4215718  
A:Accession: A01867  
A:Molecule type: protein  
A:Residues: 1-108 <LAU>  
A:Cross-references: UNIPROT:P01599  
A:Note: The C region of this chain has the Inv (3) marker  
C:Comment: This chain was isolated from a Waldenström's macroglobulin.  
C:Genetics:  
A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status predicted

Query Match 90.9%; Score 510; DB 1; Length 108;  
Best Local Similarity 92.5%; Pred. No. 2.3e-36;  
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 DIQWTPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQWTPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Qy 61 RFGSGSGTFTLTITSSLOPEDFATYCYCLOHNSYPWTFGQGTKEIK 107  
Db 61 RFGSGSGTFTLTITSSLOPEDFATYCYCLOHNSYPWTFGQGTKEIK 107

RESULT 5  
S40333  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40333  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40333  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
A:Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 495; DB 2; Length 125;  
Best Local Similarity 88.8%; Pred. No. 4.8e-35;  
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 DIQWTPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 19 DIQWTPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQSGVPS 78  
Qy 61 RFGSGSGTFTLTITSSLOPEDFATYCYCLOHNSYPWTFGQGTKEIK 107  
Db 79 RFGSGSGTFTLTITSSLOPEDFATYCYCLOHNSYPWTFGQGTKEIK 125

RESULT 6  
S41809  
Ig kappa chain V region A30 - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S41809  
R:Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zaci  
Eur. J. Immunol. 23, 2868-2875, 1993  
A:Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequence  
A:Reference number: S41809; MUID:94039386; PMID:8223863  
A:Accession: S41809  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-117 <HUB>  
A:Cross-references: EMBL:X72808; NID:g415383; PIDN:CAA51328.1; PID:g415384  
C:Genetics:  
A:Introns: 19/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 88.1%; Score 494; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5.5e-35;

```
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 23 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 82

Qy 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYP 95
Db 83 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYP 117

RESULT 7
S36269
Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36269
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36269
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: EMBL:Z18838; NID:933422; PIDN:CAA79290.1; PID:g939915
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 489; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.3e-34;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYTSTLSQGVPS 60

Qy 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCQQTSPFLTFGGTKLEIK 107

RESULT 8
S36262
Ig lambda chain V region (clone alpha-TNF-E7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36262
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36262
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: EMBL:Z18842
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 488; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 1.6e-34;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIVWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCQANSPLPTFGGTKVEIK 107
```

```
RESULT 9
S40367
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40367
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>
A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 485; DB 2; Length 127;
Best Local Similarity 88.8%; Pred. No. 3.4e-34;
Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 18 DIQWTSPLSASVGRVITTCRASQISINLYNWYQKPKAPKRLIYAASSLSQGVPS 77

Qy 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107
Db 78 RFSGSGTGTEFTLTISLSQPEDFATYCYCQSYNTPTWTFGGTKVEIK 124

RESULT 10
S40369
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40369
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40369
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PID:g441427
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 485; DB 2; Length 129;
Best Local Similarity 87.9%; Pred. No. 3.4e-34;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 22 DIQWTSPLSASVGRVITTCRAHVSNHLVWFQKPKAPKSLIYAASSLSQGVPS 81

Qy 61 RFSGSGTGTEFTLTISLSQPEDFATYCYCLOHNSYPWTFGGTKVEIK 107
Db 82 RFSGSGTGTEFTLTISLSQPEDFATYCYCQNSVPYPTFGGTKLEIK 128

RESULT 11
S40336
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40336
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
```

Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40336  
A:Molecule type: mRNA  
A:Residues: 1-124 <KLE>  
A:Cross-references: EMBL:X72446; NID:g441360; PIDN:CAA51114.1; PID:g441361  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 85.8%; Score 481.5; DB 2; Length 124;  
Best Local Similarity 88.0%; Pred. No. 6.5e-34;  
Matches 95; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 16 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 75

Qy 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGQGTKEIK 107  
Db 76 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGQGTKEIK 123

RESULT 12  
S40335  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
A:Accession: S40335  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40335  
A:Molecule type: mRNA  
A:Residues: 1-126 <KLE>  
A:Cross-references: EMBL:X72445  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 480; DB 2; Length 126;  
Best Local Similarity 85.8%; Pred. No. 8.9e-34;  
Matches 91; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IQMTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPSR 61  
Db 17 IQMTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPSR 76

Qy 62 FSGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGQGTKEIK 107  
Db 77 FSGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGQGTKEIK 122

RESULT 13  
S36279  
Ig lambda chain V region (clone alpha-THY-23) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
A:Accession: S36279  
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36279  
A:Molecule type: mRNA  
A:Status: preliminary; nucleic acid sequence not shown  
A:Residues: 1-108 <GRI>  
A:Cross-references: EMBL:Z18831; NID:g33418; PIDN:CAA79283.1; PID:g939911  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.4%; Score 479; DB 2; Length 108;  
Best Local Similarity 86.9%; Pred. No. 9.3e-34;  
Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGQGTKEIK 107  
Db 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGQGTKEIK 107

RESULT 14  
S40331  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
A:Accession: S40331  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40331  
A:Molecule type: mRNA  
A:Status: preliminary; translation not shown  
A:Residues: 1-123 <KLE>  
A:Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 473; DB 2; Length 123;  
Best Local Similarity 88.8%; Pred. No. 3.4e-33;  
Matches 95; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 17 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 76

Qy 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGQGTKEIK 107  
Db 77 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSY-PWTFGQGTKEIK 123

RESULT 15  
S40334  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
A:Accession: S40334  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40334  
A:Molecule type: mRNA  
A:Status: preliminary; translation not shown  
A:Residues: 1-132 <KLE>  
A:Cross-references: EMBL:X72444  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 473; DB 2; Length 132;  
Best Local Similarity 85.0%; Pred. No. 3.6e-33;  
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGDRTTITCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60

Db 22 DIQLTQSPFLSASIGDRVTITCRASQGINSYLAWYQQKPKAPKLLIYVASTLQSGVPS 81

Qy 61 RFGSGSGTEFTLTIISSLPEDFATYYCLOHNSYPWTFGQGTKVEIK 107

Db 82 RFGSGSGTEFTLTIISSLPEDFASYCQQFNSYPFTFGGGTKVEIR 128

Search completed: November 16, 2005, 22:04:08  
Job time : 13.7849 secs

THIS PAGE BLANK (USPTO)



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-18

Perfect score: 561

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLQNSYPWTFGGTKVEIK 107

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	521	92.9	108	1 KV1R_HUMAN	P01610 homo sapien
2	519	92.5	236	2 Q6GMW1	Q6gmw1 homo sapien
3	510	90.9	108	1 KV1G_HUMAN	P01599 homo sapien
4	477	85.0	236	2 Q6GMX8	Q6gmx8 homo sapien
5	471	84.0	108	2 Q9UL77	Q9ul77 homo sapien
6	469	83.6	108	2 Q9UL70	Q9ul70 homo sapien
7	466	83.1	108	1 KV1V_HUMAN	P04430 homo sapien
8	464	82.7	236	2 Q7Z3Y4	Q7z3y4 homo sapien
9	463	82.5	236	2 Q6PIH7	Q6pih7 homo sapien
10	455	81.1	236	2 Q6GMX9	Q6gmx9 homo sapien
11	454	80.9	244	2 Q65ZC8	Q65zc8 homo sapien
12	452	80.6	108	1 KV1H_HUMAN	P01600 homo sapien
13	450.5	80.3	107	2 Q96S9	Q96sa9 homo sapien
14	450	80.2	108	1 KV1S_HUMAN	P01594 homo sapien
15	447	79.7	108	1 KV1F_HUMAN	P01598 homo sapien
16	447	79.7	234	2 Q7Z473	Q7z473 homo sapien
17	447	79.7	236	2 Q6GMX0	Q6gmx0 homo sapien
18	446	79.5	129	1 KV1W_HUMAN	P04431 homo sapien
19	446	79.5	240	2 Q65ZC9	Q65zc9 homo sapien
20	444	79.1	236	2 Q6PIT5	Q6pit5 homo sapien
21	440	78.4	108	2 Q9UL79	Q9ul79 homo sapien
22	439	78.3	108	1 KV1L_HUMAN	P01604 homo sapien
23	438	78.1	108	1 KV1M_HUMAN	P01605 homo sapien
24	436	77.7	108	1 KV1M_HUMAN	P01607 homo sapien
25	435	77.5	108	1 KV1O_HUMAN	P01596 homo sapien
26	434.5	77.5	107	1 KV1D_HUMAN	Q9ul81 homo sapien
27	433.5	77.3	107	2 Q9UL81	Q9ul81 homo sapien
28	433	77.2	108	1 KV1C_HUMAN	P01595 homo sapien
29	433	77.2	117	1 KV1J_HUMAN	P01601 homo sapien
30	432	77.0	108	1 KV1E_HUMAN	P01597 homo sapien
31	431	76.8	108	1 KV1Y_HUMAN	P80362 homo sapien

32	431	76.8	129	1 KV1X_HUMAN	P04432 homo sapien
33	430	76.6	108	1 KV1Q_HUMAN	P01609 homo sapien
34	430	76.6	236	2 Q6PIH4	Q6pih4 homo sapien
35	426	75.9	108	1 KV1K_HUMAN	P01603 homo sapien
36	425	75.8	108	1 KV1N_HUMAN	P01606 homo sapien
37	423	75.4	108	1 KV1P_HUMAN	P01608 homo sapien
38	420	74.9	117	1 KV1J_HUMAN	P01602 homo sapien
39	419	74.7	108	1 KV1A_HUMAN	P01593 homo sapien
40	411	73.3	116	2 Q96PF6	Q96pf6 homo sapien
41	404	72.0	108	1 KV5S_MOUSE	P01652 mus musculus
42	401	71.5	108	1 KV5Q_MOUSE	P01653 mus musculus
43	401	71.5	108	1 KV5T_MOUSE	P04207 homo sapien
44	399.5	71.2	129	1 KV3H_HUMAN	P01612 homo sapien
45	396.5	70.7	109	1 KV1T_HUMAN	P01612 homo sapien

#### ALIGNMENTS

##### RESULT 1

ID KV1R\_HUMAN STANDARD; PRT; 108 AA.  
AC P01610;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-I region WEA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83273707; PubMed=6410398;  
RA Goni F., Frangione B.  
RT "Amino acid sequence of the Fv region of a human monoclonal Igm  
protein (protein WEA) with antibody activity against 3,4-pyruvylated galactose  
in Klebsiella polysaccharides K30 and K33."  
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).  
CC -I- MISCELLANEOUS: This chain was obtained from a monoclonal antibody  
against 3,4-pyruvylated galactose and isolated from a patient with  
Waldenstrom's macroglobulinemia.  
DR PIR; A01876; KIHUWE.  
DR HSPSP; P80362; IWL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region;  
KW Monoclonal antibody.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 9249B61F0945618C CRC64;

Query Match 92.9%; Score 521; DB 1; Length 108;  
Best Local Similarity 91.6%; Pred. No. 9.8e-46;  
Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASGIRNDLGTWYQKPKAPKRLIYAASSIQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASGIRNDLGTWYQKPKAPKRLIYAASSIQSGVPS 60



RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.B.,  
RA Jones S.J., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).  
RN [2].  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RE EMBL: BC073764; AAH73764.1; -.  
DR InterPro: IPR003599; Ig-like.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003597; Ig-cl.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig v.  
DR Pfam: PF07654; C1-set; 1.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IGcl; 1.  
DR SMART: SM00406; IGv; 1.  
DR PROSITE: PS00835; IG LIKE; 2.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25707 MW; 4FCB514B6559EFC9 CRC64;  
  
Query Match 85.0%; Score 477; DB 2; Length 236;  
Best Local Similarity 86.9%; Pred. No. 7.8e-41;  
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 23 DIQMTQSPSSLSASVGRVTITCRASQGISLAWYQKPKAPKRLIYAASSLSQSGVPS 82  
  
Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPWTFGGTKVEIK 107  
Db 83 RFSGSGSGTDTLTITSLQPEDPATYICQQAHSFPFTFGPGTKVDIK 129  
  
RESULT 5  
Q9UL77 PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
(Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
RE EMBL: AF035044; AAD56280.1; -.  
DR PIR: PH0863; PH0863.  
DR HSSP: P01607; 1BWW.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig v.  
DR SMART: SM00406; IGv; 1.  
DR PROSITE: PS00835; IG LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;  
  
Query Match 83.6%; Score 469; DB 2; Length 108;  
Best Local Similarity 86.0%; Pred. No. 2.2e-40;  
Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
  
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISNLYAWYQKPKPKSLIYAASSLSQSGVPS 60  
  
Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPWTFGGTKVEIK 107  
Db 61 RFSGSGSGTDTLTITSLQPEDPATYICQKINSAPRTFGPGTKDEIK 107

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
RE EMBL: AF035037; AAD56273.1; -.  
DR PIR: B49047; B49047.  
DR PIR: S34083; S34083.  
DR HSSP: P01607; 1BWW.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig v.  
DR SMART: SM00406; IGv; 1.  
DR PROSITE: PS00835; IG LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;  
  
Query Match 84.0%; Score 471; DB 2; Length 108;  
Best Local Similarity 86.9%; Pred. No. 1.3e-40;  
Matches 93; Conservative 3; Mismatches 11; Indels 0; Gaps 0;  
  
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISNLYAWYQKPKAPKRLIYAASSLSQSGVPS 60  
  
Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPWTFGGTKVEIK 107  
Db 61 RFSGSGSGTDTLTITSLQPEDPATYICQSQSYSTSWTFEGTGKVEIK 107  
  
RESULT 6  
Q9UL70 PRELIMINARY; PRT; 108 AA.  
AC Q9UL70;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
(Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
RE EMBL: AF035044; AAD56280.1; -.  
DR PIR: PH0863; PH0863.  
DR HSSP: P01607; 1BWW.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig v.  
DR SMART: SM00406; IGv; 1.  
DR PROSITE: PS00835; IG LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;  
  
Query Match 83.6%; Score 469; DB 2; Length 108;  
Best Local Similarity 86.0%; Pred. No. 2.2e-40;  
Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
  
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGINRDLGWYQKPKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISNLYAWYQKPKPKSLIYAASSLSQSGVPS 60  
  
Qy 61 RFSGSGSGTEFTLTISSLQPEDPATYICLOHNSYPWTFGGTKVEIK 107  
Db 61 RFSGSGSGTDTLTITSLQPEDPATYICQKINSAPRTFGPGTKDEIK 107



RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034141; AAH34141.1; -;  
 DR HSP; P01607; IAR2.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;  
 Query Match 82.5%; Score 463; DB 2; Length 236;  
 Best Local Similarity 86.9%; Pred. No. 2.1e-39;  
 Matches 93; Conservative 3; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 DIQWTPSPSLASVGRVITTCRASQIRNDLGVQKPKAPKRLIYAASLSQGVPS 60  
 Db 23 DIQWTPSPSLASVGRVITTCRASQIRNDLGVQKPKAPKRLIYAASLSQGVPS 82  
 QY 61 RFSGSGSGTFTLTISLQPEDFATYCYLQHSNYPWTFGGTKVEIK 107  
 Db 83 RFSGSGSGTFTLTISLQPEDFATYCYLQHSNYPWTFGGTKVEIK 129  
 RESULT 10  
 ID Q6GMX9 PRELIMINARY; PRT; 236 AA.  
 AC Q6GMX9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Heien F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Skapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073763; AAH73763.1; -;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF7 CRC64;  
 Query Match 81.1%; Score 455; DB 2; Length 236;  
 Best Local Similarity 83.2%; Pred. No. 1.4e-38;  
 Matches 89; Conservative 5; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 DIQWTPSPSLASVGRVITTCRASQIRNDLGVQKPKAPKRLIYAASLSQGVPS 60  
 Db 23 DIQWTPSPSLASVGRVITTCRASQIRNDLGVQKPKAPKRLIYAASLSQGVPS 82  
 QY 61 RFSGSGSGTFTLTISLQPEDFATYCYLQHSNYPWTFGGTKVEIK 107  
 Db 83 RFSGSGSGTFTLTISLQPEDFATYCYLQHSNYPWTFGGTKVEIK 129  
 RESULT 11  
 ID Q65ZC8 PRELIMINARY; PRT; 244 AA.  
 AC Q65ZC8;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Single-chain Fv (Fragment).  
 GN Name=scFv;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97362799; PubMed=9219263;  
 RA Kottmann R.E., Wing M.G., Winter G.;  
 RL "Complement recruitment using bispecific diabodies.";  
 RL Nat. Biotechnol. 15:629-631(1997).  
 DR EMBL; Y13057; CAA73500.1; -;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 2.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 FT NON\_TER 1 244  
 SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 80.9%; Score 454; DB 2; Length 244;  
Best Local Similarity 81.3%; Pred. No. 1.9e-38;  
Matches 87; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQWTSFSSLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
Db 137 DIQWTSFSSLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 196

Qy 61 RFGSGSGTETLTITSSLPQDFATYYCLOHNSYPWTFGQGTKEIK 107  
Db 197 RFGSGSGTETLTITSSLPQDFATYYCLOHNSYPWTFGQGTKEIK 243

RESULT 12  
KV1B\_HUMAN  
AC P01600; STANDARD; PRT; 108 AA.  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.

RA MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups";  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; A01868; K1HUHU.  
DR PDB; 1P6L; X-ray; L=1-108.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULETD 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 80.6%; Score 452; DB 1; Length 108;  
Best Local Similarity 84.1%; Pred. No. 1.2e-38;  
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQWTSFSSLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQWTSFSSLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPQVLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTETLTITSSLPQDFATYYCLOHNSYPWTFGQGTKEIK 107  
Db 61 RFGSGSGTETLTITSSLPQDFATYYCLOHNSYPWTFGQGTKEIK 107

RESULT 13

Q96SA9  
ID Q96SA9 PRELIMINARY; PRT; 107 AA.  
AC Q96SA9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98375893; PubMed=9712075;  
RA Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal antibodies from rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes";  
RL J. Immunol. 161:2020-2031 (1998).  
DR EMBL; U96396; AB868785.1; -.  
DR PIR; B49047; B49047.  
DR PIR; PH0867; PH0867.  
DR PIR; S16840; S16840.  
DR PIR; S31977; S31977.  
DR PIR; S34083; S34083.  
DR PIR; S34086; S34086.  
DR HSPF; P01607; 1BWW.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; IGV.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1 107  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 80.3%; Score 450.5; DB 2; Length 107;  
Best Local Similarity 86.9%; Pred. No. 1.7e-38;  
Matches 93; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

Qy 1 DIQWTSFSSLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQWTSFSSLSASVGDRTTTCRASQIRNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTETLTITSSLPQDFATYYCLOHNSYPWTFGQGTKEIK 107  
Db 61 RFGSGSGTETLTITSSLPQDFATYYCLOHNSYPWTFGQGTKEIK 106

RESULT 14  
KV1B\_HUMAN  
ID KV1B\_HUMAN STANDARD; PRT; 108 AA.  
AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig kappa chain V-I region AU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=72189444; PubMed=5028201;  
RA Schiechl H., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au)";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehlfhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,

RA Schwager P., Steigemann W., Schramm H.J.;  
RT "The structure determination of the variable portion of the Bence-  
RL Jones protein Au.";  
CC -1- MISCELLANEOUS: Mech. 1:139-146(1975).  
CC molecular replacement methods using the known structure of the V  
region of the kappa chain REI.  
CC -1- MISCELLANEOUS: The structure of the V region was determined by  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PR; A91653; KIHUAV.

DR PDB; 1JVS; X-ray; A=1-107.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.

KW 3D-structure; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin V region.

FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DOMAIN 23 88  
FT DISULFID 23 88  
FT STRAND 4 5  
FT STRAND 10 13  
FT TURN 15 16  
FT STRAND 19 25  
FT TURN 30 31  
FT STRAND 33 38  
FT TURN 40 41  
FT STRAND 44 49  
FT TURN 50 52  
FT STRAND 53 54  
FT TURN 56 57  
FT TURN 60 61  
FT STRAND 62 67  
FT TURN 68 69  
FT STRAND 70 75  
FT HELIX 80 82  
FT STRAND 85 90  
FT STRAND 97 98  
FT STRAND 102 106  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6F99 CRC64;

Query Match 80.2%; Score 450; DB 1; Length 108;  
Best Local Similarity 81.3%; Pred. No. 1.9e-38;  
Matches 87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQGVPS 60  
Db 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTISLQPEDPATYCYCLOHNSYPWTFGGQTKVEIK 107  
Db 61 RFGSGSGTFTLTISLQPEDPATYCYCLOHNSYPWTFGGQTKVEIK 107

## RESULT 15

KVIF\_HUMAN  
ID KVIF\_HUMAN STANDARD; PRT; 108 AA.  
AC P01598;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-I region EU.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN RN  
RX MEDLINE=71064023; PubMed=5489770;  
RA Gattlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
RL acid sequence of the light chain.";  
RL Biochemistry 9:3155-3161(1970).  
RN [2]  
RN RN  
RP DISULFIDE BOND.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RL Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.  
DR PIR; A90562; KIHUEU.

DR HSP; P01607; IBMW.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.

KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 79.7%; Score 447; DB 1; Length 108;  
Best Local Similarity 82.2%; Pred. No. 3.9e-38;  
Matches 88; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQGVPS 60  
Db 1 DIQWTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTISLQPEDPATYCYCLOHNSYPWTFGGQTKVEIK 107  
Db 61 RFGSGSGTFTLTISLQPEDPATYCYCLOHNSYPWTFGGQTKVEIK 107

Search completed: November 16, 2005, 22:01:52  
Job time : 60.9908 secs

THE FINE DENT (USPTO)



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357A-18  
Perfect score: 561  
Sequence: 1 DIQWTSPLSASVGDVRT.....CLQHSYPWTFGGTKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	522	91.0	107	3	US-09-240-274-29
2	501	89.3	107	2	US-07-934-373C-18
3	501	89.3	107	4	US-08-437-642B-18
4	501	89.3	107	4	US-08-146-206C-18
5	501	89.3	107	4	US-09-648-067A-14
6	501	89.3	107	4	US-09-705-686-18
7	501	89.3	107	4	US-09-705-392A-18
8	501	89.3	107	4	US-09-705-398-18
9	501	89.3	107	5	PCT-US93-07832-18
10	501	89.3	108	3	US-08-974-899-3
11	501	89.3	108	4	US-09-795-798-3
12	500	89.1	108	2	US-08-378-939-32
13	500	89.1	108	2	US-08-378-939-34
14	496	88.4	236	4	US-08-859-053-30
15	487	86.8	107	3	US-08-599-226-1
16	487	86.8	107	3	US-09-125-098-1
17	487	86.8	107	4	US-09-540-018-1
18	486	86.6	107	3	US-09-599-226-9
19	486	86.6	107	3	US-09-125-098-9
20	486	86.6	107	4	US-09-540-018-9
21	485	86.5	109	2	US-07-934-373C-3
22	485	86.5	109	3	US-08-437-642B-3
23	485	86.5	109	4	US-08-146-206C-3
24	485	86.5	109	4	US-09-705-686-3
25	485	86.5	109	4	US-09-705-392A-3
26	485	86.5	109	4	US-09-705-398-3
27	485	86.5	109	5	PCT-US93-07832-3

28	484	86.3	107	3	US-08-871-488A-18	Sequence 18, Appl
29	484	86.3	109	3	US-09-025-769B-28	Sequence 28, Appl
30	484	86.3	109	3	US-09-025-769B-43	Sequence 43, Appl
31	484	86.3	109	4	US-09-490-070A-28	Sequence 28, Appl
32	484	86.3	109	4	US-09-490-070A-43	Sequence 43, Appl
33	484	86.3	109	4	US-09-490-153-28	Sequence 28, Appl
34	484	86.3	109	4	US-09-490-153-43	Sequence 43, Appl
35	484	86.3	109	4	US-09-490-324-28	Sequence 28, Appl
36	484	86.3	109	4	US-09-490-324-43	Sequence 43, Appl
37	483	86.1	236	1	US-08-157-101A-5	Sequence 5, Appl
38	481	85.7	107	2	US-07-934-373C-17	Sequence 17, Appl
39	481	85.7	107	3	US-08-437-642B-17	Sequence 17, Appl
40	481	85.7	107	4	US-08-146-206C-17	Sequence 17, Appl
41	481	85.7	107	4	US-09-705-686-17	Sequence 17, Appl
42	481	85.7	107	4	US-09-705-392A-17	Sequence 17, Appl
43	481	85.7	107	4	US-09-705-398-17	Sequence 17, Appl
44	481	85.7	107	5	PCT-US93-07832-17	Sequence 17, Appl
45	481	85.7	108	2	US-08-378-939-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-09-240-274-29  
; Sequence 29, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain F01  
US-09-240-274-29

Query Match 93.0%; Score 522; DB 3; Length 107;  
Best Local Similarity 93.3%; Pred. No. 9.6e-41;  
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy	3	QMTQSPSSLSASVGDVRTITCRASQGRNDLGMVQKPGKAPKRLIYAASSLQSGVPSRF	62
Db	2	ELTQSPSSLSASVGDVRTITCRASQGRNDLGMVQKPGKAPKRLIYATSSLQSGVPSRF	61
Qy	63	SGSGSGTEFTLTISLQPEDFATYICLQHSYPWTFGGTKVEIK	107
Db	62	SGSGSGTEFTLTINSLQPEDSATYICLQHSFPWTFGGTKVEIK	106

RESULT 2  
US-07-934-373C-18  
; Sequence 18, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way

```
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1991
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-18

Query Match      89.3%; Score 501; DB 2; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGRVTTTCRASQIRNDLGHYQOKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTSPSSLSASVGRVTTTCRASQIRNDLGHYQOKGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSVPWTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSVPWTFGGTKVEIK 107

RESULT 3
US-08-437-642B-18
; Sequence 18, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1991
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-18

Query Match      89.3%; Score 501; DB 3; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGRVTTTCRASQIRNDLGHYQOKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTSPSSLSASVGRVTTTCRASQIRNDLGHYQOKGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSVPWTFGGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPQEDFATYYCLOHNSVPWTFGGTKVEIK 107

RESULT 4
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-18
Query Match      89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVITTCRASQISNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTFTLTITISSLPQEDPATYCYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITISSLPQEDPATYCYCQYNSLPWTFGGQTKVEIK 107

RESULT 5
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14
Query Match      89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVITTCRASQISNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTFTLTITISSLPQEDPATYCYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITISSLPQEDPATYCYCQYNSLPWTFGGQTKVEIK 107

RESULT 6
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-Nov-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18
Query Match      89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVITTCRASQISNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTFTLTITISSLPQEDPATYCYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITISSLPQEDPATYCYCQYNSLPWTFGGQTKVEIK 107

RESULT 7
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-Nov-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
```

```
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-Nov-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18
Query Match      89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
DB 1 DIQWTQSPSSLSASVGRVITTCRASQISNYLAWYQKPKAPKRLIYAASSLSQSGVPS 60

QY 61 RFGSGSGTFTLTITISSLPQEDPATYCYCLOHNSYPWTFGGQTKVEIK 107
DB 61 RFGSGSGTFTLTITISSLPQEDPATYCYCQYNSLPWTFGGQTKVEIK 107

RESULT 7
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-Nov-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
```

```
/
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P0709PID1 REVISED
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1994
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18

Query Match      89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISNYLAWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTFTLTITSSIQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFGSGSGTFTLTITSSIQPEDFATYYCQYNSLPWTFGGQTKVEIK 107

RESULT 8
US-09-705-398-18
; Sequence 18, Application US/09705398
; Patent No. 6800738
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; PRESTA, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18

Query Match      89.3%; Score 501; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISNYLAWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTFTLTITSSIQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFGSGSGTFTLTITSSIQPEDFATYYCQYNSLPWTFGGQTKVEIK 107

RESULT 9
PCT-US93-07832-18
; Sequence 18, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-18

Query Match      89.3%; Score 501; DB 5; Length 107;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWYQKPKGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSIISNYLAWYQKPKGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTFTLTITSSIQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFGSGSGTFTLTITSSIQPEDFATYYCQYNSLPWTFGGQTKVEIK 107

RESULT 10
US-08-974-899-3
```

```
; Sequence 3, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-3

Query Match      89.3%; Score 501; DB 3; Length 108;
Best Local Similarity 90.7%; Pred. No. 8.1e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGWYQKFKGKAPKRLIYAASSLSQGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQWTSPLSASVGRVITTCRASQISNYLAWYQKFKGKAPKRLIYAASSLSQGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFGSGSGTFTLTITISLQPEDFATYVCLQHSYPTWTFGGTKVEIK 107
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTFTLTITISLQPEDFATYVCCQVNSLPWTFGGTKVEIK 107
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-795-798-3
; Sequence 3, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
; US-09-795-798-3

Query Match      89.3%; Score 501; DB 4; Length 108;
Best Local Similarity 90.7%; Pred. No. 8.1e-39;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGRVITTCRASQIRNDLGWYQKFKGKAPKRLIYAASSLSQGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQWTSPLSASVGRVITTCRASQISNYLAWYQKFKGKAPKRLIYAASSLSQGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RFGSGSGTFTLTITISLQPEDFATYVCLQHSYPTWTFGGTKVEIK 107
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTFTLTITISLQPEDFATYVCCQVNSLPWTFGGTKVEIK 107
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-08-378-939-32
; Sequence 32, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-32

Query Match      89.1%; Score 500; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 1e-38;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQGISNNLAWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTITSSLPQDFATYYCLOHNSYPWTFGQGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPQDFATYYCQDNSYPFTFGGGTKVEIK 107

RESULT 13
US-08-378-939-34
; Sequence 34, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-34

Query Match      89.1%; Score 500; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 1e-38;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQGISNNLAWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTITSSLPQDFATYYCLOHNSYPWTFGQGTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLPQDFATYYCQDNSYPFTFGGGTKVEIK 107
```

```
RESULT 14
US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Query Match      88.4%; Score 496; DB 4; Length 236;
Best Local Similarity 89.7%; Pred. No. 5.3e-38;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 23 DIQMTQSPSSVSASVGDRTVITTCRASQGISRLAWYQKPGKAPKRLIYVASSLSQGVPS 82

Qy 61 RFGSGSGTFTLTITSSLPQDFATYYCLOHNSYPWTFGQGTKVEIK 107
Db 83 RFGSGSGTFTLTITSSLPQDFATYYCQQANSFPWTFGQGTKVEIK 129

RESULT 15
US-08-599-226-1
; Sequence 1, Application US/08599226
; Patent No. 6090382
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
US-08-599-226-1

Query Match      86.8%; Score 487; DB 3; Length 107;
Best Local Similarity 88.8%; Pred.No.1.5e-37;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLASVGDVRVTITCRASQGIKNDLGWYQOKPKAPKRLIYAASSLQSGVPS 60
Db 1 DIQWTQSPSSLASVGDVRVTITCRASQGIKNDLGWYQOKPKAPKRLIYAASSLQSGVPS 60

Qy 61 RFGSGSGGTFTLTITSSLPEDPATYICLQHNSTPWTFGQGTKEIK 107
Db 61 RFGSGSGGTFTLTITSSLPEDPATYICLQHNSTPWTFGQGTKEIK 107
```

Search completed: November 16, 2005, 22:07:19  
Job time : 18.1939 secs

THIS PAGE BLANK (SEPTO)



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds  
(without alignments)  
681.481 Million cell updates/sec

Title: US-10-660-357A-18

Perfect score: 561

Sequence: 1 DIQWTSPLSASVGRVT.....CLOHNSYPWTFGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep:\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep:\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561	100.0	107	14	US-10-330-613-18
2	561	100.0	107	14	US-10-330-530-18
3	561	100.0	107	14	US-10-041-860-26
4	561	100.0	107	14	US-10-041-860-28
5	561	100.0	107	14	US-10-041-860-36
6	561	100.0	107	14	US-10-041-860-231
7	561	100.0	107	14	US-10-041-860-232
8	561	100.0	107	14	US-10-041-860-234
9	561	100.0	107	14	US-10-041-860-266
10	561	100.0	107	14	US-10-041-860-268
11	561	100.0	107	14	US-10-041-860-316
					Sequence 18, Appl
					Sequence 18, Appl
					Sequence 26, Appl
					Sequence 28, Appl
					Sequence 36, Appl
					Sequence 231, App
					Sequence 232, App
					Sequence 234, App
					Sequence 266, App
					Sequence 268, App
					Sequence 316, App

12	561	100.0	107	14	US-10-041-860-340	Sequence 340, App
13	561	100.0	107	15	US-10-309-762-166	Sequence 166, App
14	561	100.0	107	16	US-10-660-357-18	Sequence 18, Appl
15	561	100.0	107	16	US-10-665-383-32	Sequence 32, Appl
16	561	100.0	107	16	US-10-665-383-36	Sequence 36, Appl
17	561	100.0	107	16	US-10-665-383-52	Sequence 52, Appl
18	561	100.0	107	17	US-10-727-155-274	Sequence 274, App
19	561	100.0	107	17	US-10-727-155-307	Sequence 307, App
20	561	100.0	236	15	US-10-038-591-52	Sequence 52, Appl
21	561	100.0	236	16	US-10-775-444A-52	Sequence 52, Appl
22	561	100.0	236	17	US-10-917-073A-6	Sequence 6, Appl
23	558	99.5	107	14	US-10-041-860-265	Sequence 265, App
24	556	99.1	107	17	US-10-727-155-64	Sequence 64, Appl
25	551	98.2	107	14	US-10-041-860-309	Sequence 309, App
26	549	97.9	107	17	US-10-727-155-16	Sequence 16, Appl
27	549	97.9	107	17	US-10-727-155-260	Sequence 260, App
28	549	97.9	236	15	US-10-038-591-48	Sequence 48, Appl
29	549	97.9	236	16	US-10-775-444A-48	Sequence 48, Appl
30	548	97.7	107	14	US-10-041-860-24	Sequence 24, Appl
31	548	97.7	107	14	US-10-041-860-230	Sequence 230, App
32	548	97.7	107	14	US-10-041-860-264	Sequence 264, App
33	548	97.7	107	14	US-10-041-860-303	Sequence 303, App
34	548	97.7	107	16	US-10-665-383-28	Sequence 28, Appl
35	547	97.5	107	17	US-10-727-155-60	Sequence 60, Appl
36	546	97.3	107	18	US-10-822-306A-16	Sequence 16, Appl
37	546	97.3	108	17	US-10-726-332-211	Sequence 211, App
38	545	97.1	107	15	US-10-309-762-53	Sequence 53, Appl
39	545	97.1	107	15	US-10-309-762-56	Sequence 56, Appl
40	542	96.6	152	17	US-10-644-277-96	Sequence 96, Appl
41	541	96.4	107	14	US-10-330-613-14	Sequence 14, Appl
42	541	96.4	107	14	US-10-330-530-14	Sequence 14, Appl
43	541	96.4	107	14	US-10-041-860-18	Sequence 18, Appl
44	541	96.4	107	14	US-10-041-860-233	Sequence 233, App
45	541	96.4	107	14	US-10-041-860-267	Sequence 267, App

ALIGNMENTS

RESULT 1  
US-10-330-613-18  
; Sequence 18, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-18

Query Match 100.0%; Score 561; DB 14; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-39;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DIQWTSPLSASVGRVTITCRASQIGIRNDLGMWQKPKAPKRLIYAASSLSQGVPS	60
Db	1	DIQWTSPLSASVGRVTITCRASQIGIRNDLGMWQKPKAPKRLIYAASSLSQGVPS	60
Qy	61	RFGSGSGTEFTLTITSSLPQDEFATYVCLQHNSYPWTFGGTKVEIK	107
Db	61	RFGSGSGTEFTLTITSSLPQDEFATYVCLQHNSYPWTFGGTKVEIK	107

RESULT 2

```
US-10-330-530-18
; Sequence 18, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-18

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107

RESULT 3
US-10-041-860-26
; Sequence 26, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-26

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107

RESULT 4
US-10-041-860-28
; Sequence 28, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-28

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107

RESULT 5
US-10-041-860-36
; Sequence 36, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-36

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107
```

```
US-10-041-860-36
; Sequence 36, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-36

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107

RESULT 6
US-10-041-860-36
; Sequence 36, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-36

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLGMWQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYYCLOHNSYPWTFGGTKVEIK 107
```

```
Db 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
RESULT 6
US-10-041-860-231
; Sequence 231, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-231

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 7
US-10-041-860-232
; Sequence 232, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-232

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 8
US-10-041-860-233
; Sequence 233, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-233

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 9
US-10-041-860-266
; Sequence 266, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 266
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-266

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
```

```
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 8
US-10-041-860-234
; Sequence 234, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 234
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-234

Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLQWYQKPKAPKRLIYAASLSQSGVPS 60
|||||
Qy 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||
Db 61 RFSGSGGTFTLTISLQPEDFATYYCLOHNSYPWTFGGTKVEIK 107
|||||

RESULT 9
US-10-041-860-266
; Sequence 266, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 266
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-266
```

```
Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
    |||||
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
    |||||

Qy 61 RFGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
    |||||
Db 61 RFGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
    |||||

RESULT 10
US-10-041-860-268
; Sequence 268, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-268

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
    |||||
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
    |||||

Qy 61 RFGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
    |||||
Db 61 RFGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
    |||||

RESULT 11
US-10-041-860-316
; Sequence 316, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316
```

```
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-316

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
    |||||
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
    |||||

Qy 61 RFGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
    |||||
Db 61 RFGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
    |||||

RESULT 12
US-10-041-860-340
; Sequence 340, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-340

Query Match      100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPLSASVGDRTTTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
    |||||
Db 1 DIQWTSPLSASVGDRTTTCRASQIRNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
    |||||

Qy 61 RFGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
    |||||
Db 61 RFGSGSGTEFTLTITSSSQPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
    |||||

RESULT 13
US-10-309-762-166
; Sequence 166, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
```

```
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-166

Query Match      100.0%; Score 561; DB 15; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 14
US-10-660-357-18
; Sequence 18, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: AGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-18

Query Match      100.0%; Score 561; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

RESULT 15
US-10-665-383-32
; Sequence 32, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochelle, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: AGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
```

```
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-32

Query Match      100.0%; Score 561; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGMWQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107
Db 61 RFGSGSGTFTLTITSSLSQPEDFATYYCLOHNSYPWTFGGQTKVEIK 107

Search completed: November 16, 2005, 23:05:42
Job time : 66.6949 secs
```

UNITED STATES PATENT AND TRADEMARK OFFICE (USPTO)

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 64.8088 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-22

Perfect score: 590

Sequence: 1 DIVMTQSPDSLAVSISGERAT.....COQYSTRPSCFGTGMVEIK 113

Scoring table: BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	113	7	Adc99793 Anti-huma
2	590	100.0	113	7	Adf05397 Anti-MUC1
3	590	100.0	113	7	Adf09835 Human ant
4	556	94.2	133	1	Aap80894 V region
5	550	93.2	114	8	Adp36363 Intracell
6	549	93.1	122	8	Adi26708 Human ant
7	546	92.5	114	8	Adp03687 Human ant
8	546	92.5	114	8	Adp03713 Human ant
9	546	92.5	120	4	Aag65565 Amino aci
10	546	92.5	135	3	Aab03714 Immunoglo
11	546	92.5	135	6	Ada47343 Human ant
12	546	92.5	135	7	Adb72875 Human AAA
13	546	92.5	135	8	Adp88458 Human ant
14	546	92.5	135	8	Adq87927 Human HSI
15	546	92.5	135	8	Adp03811 Human ant
16	544	92.2	114	8	Ado32154 Mouse ant
17	544	92.2	114	8	Adq75236 Immunoglo
18	544	92.2	155	2	Aaw32483 Kappa lig
19	544	92.2	155	2	Aay06912 Human var
20	544	92.2	342	2	Aaw32482 Growth fa
21	544	92.2	342	2	Aay06909 TLHL amin
22	544	92.2	495	2	Aaw32480 Growth fa
23	544	92.2	495	2	Aay06908 CATAB-TEV
24	543	92.0	114	8	Adp03705 Human ant
25	543	92.0	114	8	Adp03709 Human ant

26	543	92.0	114	8	ADP03683	Adp03683 Human ant
27	543	92.0	114	8	ADP03695	Adp03695 Human ant
28	543	92.0	179	8	ADK52434	Adk52434 Human ant
29	542	91.9	252	8	ADO58062	Ado58062 S2 cell d
30	541	91.7	240	4	AAU00815	Aau00815 Human Imm
31	540	91.5	113	8	ADP03723	Adp03723 Human ant
32	540	91.5	119	5	ABSO7172	Abso7172 ebvHlgM M
33	540	91.5	119	8	ADI26660	Adi26660 Human ant
34	540	91.5	264	5	ABP43142	Abp43142 Human ova
35	540	91.5	283	8	ADP03815	Adp03815 Human ant
36	539.5	91.4	115	7	ADL91336	Adl91336 VL chain
37	539	91.4	114	2	AAR30144	Aar30144 MAB GAH v
38	539	91.4	114	6	ABP98692	Abp98692 Human GAH
39	539	91.4	114	6	ABP98684	Abp98684 Human GAH
40	539	91.4	114	7	ADG43870	Adg43870 Human pro
41	539	91.4	114	8	ADP03701	Adp03701 Human ant
42	539	91.4	114	8	ADQ28267	Adq28267 Method of
43	538	91.2	113	6	ABJ18724	Abj18724 Antibody
44	538	91.2	114	6	ABJ18682	Abj18682 Antibody
45	538	91.2	115	2	AAW27546	Aaw27546 Human AB

ALIGNMENTS

RESULT 1  
ADC99793  
ID ADC99793 standard; protein; 113 AA.  
XX  
AC ADC99793;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 22.  
XX  
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.  
XX  
OS Homo sapiens.  
XX  
FN WO2003057838-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041581.  
XX  
PR 28-DEC-2001; 2001US-0346299P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
DR WPI; 2003-587113/55.  
DR N-PSDB; ADC99795.  
XX  
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.  
XX  
PS Claim 3; SEQ ID NO 22; 78pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody

```
CC light chain protein of the invention.
XX
SQ Sequence 113 AA;

Query Match      100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
OY 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113
DB 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113

RESULT 2
ID ADD05397 standard; protein; 113 AA.
XX
AC ADD05397;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 22.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
DR N-PSDB; ADD05399.
XX
PS Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 3; SEQ ID NO 22; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
SQ Sequence 113 AA;

Query Match      100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
OY 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113
DB 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113

RESULT 3
ID ADF09835 standard; protein; 113 AA.
XX
AC ADF09835;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #6.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-598367/56.
DR N-PSDB; ADF09837.
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumour
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 3; SEQ ID NO 22; 83pp; English.
XX
CC The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 113 AA;

Query Match      100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDSLAVSLGERATIIICKSQSILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
OY 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113
DB 61 ESGVPARFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113
```







```
QY 1 DIVMTQSPDLSAVSLGERATITICKSSQSYLYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
QY 61 ESGVPPRFGSGSGTDTLTITSLQAEADVAVYVYCCQYVSTPRSGGQGTWVEIK 113
DB 61 ESGVPPRFGSGSGTDTLTITSLQAEADVAVYVYCCQYVSTPRSGGQGTWVEIK 113

RESULT 8
ADP03713
ID ADP03713 standard; protein; 114 AA.
XX
AC ADP03713;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human antibody related protein sequence, SEQ ID 86.
XX
KW Cytostatic; Antiarteriosclerotic; Antiinflammatory; Immunosuppressive;
KW human; antibody; cancer lesion; arteriosclerosis; inflammatory disease;
KW autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN WO2004048571-A1.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-JP014919.
XX
PR 22-NOV-2002; 2002JP-00339241.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PA (PHAR-) PHARMALOGICALS RES PTE LTD.
XX
PI Tsuchiya M, Suzuki M, Yoshida K, Fujii E, Matsubara K, Tsunoda H;
XX
DR WPI; 2004-450382/42.
XX
DR N-PSDB; ADP03712.
XX
PT Isolating polynucleotide that encodes antibody which acts against
PT lesioned tissue, involves isolating B cells that is infiltrated into
PT lesioned tissue, and acquiring polynucleotide that encodes antibody from
PT isolated B cells.
XX
PS Example 4; SEQ ID NO 86; 200pp; Japanese.
XX
CC The present invention relates to novel antibody sequences, which acts
CC against lesioned tissue. Also claimed is a method (M1) for isolating B
CC polynucleotide encoding the antibodies, which involves (a) isolating B
CC cells that is infiltrated into lesioned tissue, and (b) acquiring B
CC polynucleotide that encodes an antibody from the isolated B cells. The
CC antibodies are useful for treating cancer lesions, arteriosclerosis,
CC inflammatory disease or autoimmune disease. The present sequence was used
CC to illustrate the invention.
XX
SQ Sequence 114 AA;
```

```
Query Match 92.5%; Score 546; DB 8; Length 114;
Best Local Similarity 92.0%; Pred. No. 1.4e-38;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATITICKSSQSYLYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
QY 61 ESGVPPRFGSGSGTDTLTITSLQAEADVAVYVYCCQYVSTPRSGGQGTWVEIK 113
DB 61 ESGVPPRFGSGSGTDTLTITSLQAEADVAVYVYCCQYVSTPRSGGQGTWVEIK 113
```

```
RESULT 9
AAG65565
ID AAG65565 standard; protein; 120 AA.
XX
AC AAG65565;
XX
DT 30-NOV-2001 (first entry)
XX
DE Amino acid sequence of protein seq Id No. 90.
XX
KW Gene library; immunoglobulin; antibody library; human.
XX
OS Homo sapiens.
XX
PN WO200162907-A1.
XX
PD 30-AUG-2001.
XX
PF 22-FEB-2001; 2001WO-JP001298.
XX
PR 22-FEB-2000; 2000JP-00050543.
XX
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX
DR WPI; 2001-565420/63.
XX
DR N-PSDB; AAH47729.
XX
PT Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX
PS Examples; p 165; 181pp; Japanese.
XX
CC The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries
XX
SQ Sequence 120 AA;

Query Match 92.5%; Score 546; DB 4; Length 120;
Best Local Similarity 92.0%; Pred. No. 1.4e-38;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATITICKSSQSYLYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
QY 61 ESGVPPRFGSGSGTDTLTITSLQAEADVAVYVYCCQYVSTPRSGGQGTWVEIK 113
DB 61 ESGVPPRFGSGSGTDTLTITSLQAEADVAVYVYCCQYVSTPRSGGQGTWVEIK 113

RESULT 10
AAB03714
ID AAB03714 standard; protein; 135 AA.
XX
AC AAB03714;
XX
DT 04-OCT-2000 (first entry)
XX
DE Immunoglobulin kappa2 amino acid sequence fragment.
XX
KW Aortic aneurysm-associated antigen protein; AABP; microfibrillar protein;
KW abdominal aortic aneurysm disease; treatment; detect; tolerance;
KW immunoglobulin kappa; 19K.
```

```
XX OS Unidentified.
XX PN US6048704-A.
XX PD 11-APR-2000.
XX PD 07-MAR-1997; 97US-00812586.
XX PF 07-MAR-1996; 96US-0012976P.
XX PR (UYCO ) UNIV COLUMBIA NEW YORK.
XX PA Tilson MD;
XX PI WPI; 2000-316895/27.
XX DR Isolated microfibrillar protein for alleviating abdominal aortic aneurysm
XX PT disease is purified from human aortic tissue and binds immunoreactively
XX PT with immunoglobulin.
XX PS Example 3; Col 30; 70pp; English.
XX CC The present invention relates to an isolated microfibrillar protein of
XX CC approximately 40kD. The protein is isolated from human aortic tissue and
XX CC binds immunoreactively with immunoglobulin purified from human abdominal
XX CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic
XX CC aneurysm-associated antigenic protein (AAAP). The protein is capable of
XX CC forming a disulphide bonded dimer. The protein is immunoreactive with
XX CC human kappa immunoglobulin. Also included in the invention are
XX CC recombinantly produced human AAA proteins. AAAP shows regions of homology
XX CC with the bovine microfibril associated glycoprotein MFAP-4 and also with
XX CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful
XX CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
XX CC presence of AAA-associated immunoglobulin bound to the human aortic
XX CC tissue. Antibodies directed against AAAP can be used to detect AAA
XX CC disease. The recombinant protein can be used to induce tolerance to
XX CC antigenic AAA protein in the subject e.g. human. This sequence represents
XX CC an immunoglobulin kappa2 amino acid sequence. The sequence shares
XX CC homology with the AAAP of the invention, it was used to identify and
XX CC characterise AAAP
XX SQ Sequence 135 AA;
XX Query Match 92.5%; Score 546; DB 3; Length 135;
XX Best Local Similarity 92.9%; Pred. No. 1.6e-38;
XX Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIVMTQSPDLSAVSLGERATICKSSQSIYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSIYSSNNKNYLAWYQKPGQPPKLLIYWASTR 80
QY 61 ESGVPARFSGSGGTDTFTLTINSIQAEDVAVYVYCCQYVSTPRSGQGTWVEIK 113
DB 81 ESGVPDRFSGSGGTDTFTLTISLSQAEDVAVYVYCCQYVSTPPMFQGTQKVEIK 133
RESULT 11
ADA47343
ID ADA47343 standard; protein; 135 AA.
XX AC ADA47343;
XX DT 20-NOV-2003 (first entry)
XX DE Human antibody H5IGKAW light chain #SEQ ID 41.
XX KW Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;
XX KW graft rejection; autoimmune disease; humanised.
XX OS Homo sapiens.
XX PN WO2002102853-A2.
XX PD 27-DEC-2002.
XX PF 14-JUN-2002; 2002WO-GB002796.
XX PR 14-JUN-2001; 2001GB-00014517.
XX PR 20-SEP-2001; 2001GB-00022724.
XX PR 19-OCT-2001; 2001US-0345194P.
XX PR 18-APR-2002; 2002US-0373470P.
XX PR 18-APR-2002; 2002US-0373471P.
XX XX (ISIS-) ISIS INNOVATION LTD.
XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX PA (TOLE-) TOLERRX INC.
XX XX Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;
XX PI Ringler D, Cobbold S, Winsor-Hines D;
XX XX WPI; 2003-175228/17.
XX DR Treating a primate to induce tolerance to at least one antigen, useful
XX PT for inhibiting graft rejection or treating an autoimmune disease,
XX PT comprising administering a TRX1 antibody to reduce the amount of CD4+
XX PT CD25+ cells produced.
XX PS Example 1; Page 22; 131pp; English.
XX CC The invention relates to a method for treating a primate to induce
XX CC tolerance to at least one antigen. The method of the invention comprises
XX CC administering at least one compound which when in a primary mixed
XX CC lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells
XX CC produced. The preferred compound is a humanised antibody or its fragment,
XX CC that does not bind to the Fc receptor, and includes CDRs that are free of
XX CC a glycosylation site. The method of the invention is useful for inducing
XX CC tolerance to at least one antigen, specifically for inhibiting,
XX CC ameliorating or reducing an immune response to an antigen. The antibody
XX CC is useful for manufacturing a medicament for inducing tolerance to an
XX CC antigen (possibly in the form of a vaccine), for inhibiting an immune
XX CC response, for inhibiting the rejection of a graft (such as an organ) in a
XX CC human patient, and for treating an autoimmune disease. The current
XX CC sequence represents the human antibody H5IGKAW light chain that was used
XX CC in an example from the invention.
XX SQ Sequence 135 AA;
XX Query Match 92.5%; Score 546; DB 6; Length 135;
XX Best Local Similarity 92.9%; Pred. No. 1.6e-38;
XX Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIVMTQSPDLSAVSLGERATICKSSQSIYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSIYSSNNKNYLAWYQKPGQPPKLLIYWASTR 80
QY 61 ESGVPARFSGSGGTDTFTLTINSIQAEDVAVYVYCCQYVSTPRSGQGTWVEIK 113
DB 81 ESGVPDRFSGSGGTDTFTLTISLSQAEDVAVYVYCCQYVSTPPMFQGTQKVEIK 133
RESULT 12
ADB72875
ID ADB72875 standard; protein; 135 AA.
XX AC ADB72875;
XX XX 04-DEC-2003 (first entry)
XX DT Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:43.
XX DE Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;
XX KW AAA-associated immunoglobulin 40kDa protein.
XX OS Homo sapiens.
XX PN
```

```
PN US6537769-B1.
XX
XX 25-MAR-2003.
XX
XX 28-MAR-2000; 2000US-00535832.
XX
XX 07-MAR-1996; 96US-0012976P.
XX 07-MAR-1997; 97US-00812586.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Tilson MD;
XX
XX WPI; 2003-687181/65.
XX
XX Purified protein useful in diagnosing abdominal aortic aneurysm disease
XX in subject, e.g. human, contains specified amino acids.
XX
XX Disclosure; Col 73-76; 67pp; English.
XX
XX The present invention relates to the isolation of a protein approximately
XX 40kDa which is purified from human aortic tissue. The protein is
XX immunoreactive with abdominal aortic aneurysms(AAA)-associated
XX immunoglobulin. The protein is useful for diagnosing AAA disease in a
XX subject, e.g. human, by administering the protein or a composition
XX comprising the protein. The inventive protein is capable of forming a
XX disulphide-bonded dimer of 80 kDa. The present sequence of unknown
XX function is given in the Sequence Listing but is not mentioned elsewhere
XX in the specification.
XX
XX Sequence 135 AA;

Query Match          92.5%; Score 546; DB 7; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.6e-38;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSLYSNNKNYLGWYQKPGQPKLLIYWASTR 60
DB 21 DIVMTQSPDLSAVSLGERATITCKSSQSLYSNNKNYLAWYQKPGQPKLLIYWASTR 80
QY 61 ESGVPARFSGSGGTFTLTINSQAEDVAVYCOQYVSTPRSGGTWVEIK 113
DB 81 ESGVDRFSGSGGTFTLTISLSQAEDVAVYCOQYVSTPPMFGGQTKVEIK 133

RESULT 13
ADP88458
ID ADP88458 standard; protein; 135 AA.
XX
XX ADP88458;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human antibody H5IGKAW VL SEQ ID NO: 35.
XX
XX immunosuppressive; transplant rejection; antigen tolerance; antibody;
XX TRX1; human; H5IGKAW.
XX
XX Homo sapiens.
XX
XX WO2004052398-A1.
XX
XX 24-JUN-2004.
XX
XX 09-DEC-2003; 2003WO-US039165.
XX
XX 09-DEC-2002; 2002US-0431839P.
XX
XX (TOLE-) TOLERRX INC.
XX
XX Windsor-Hines D, Rao P, Ringler DJ;
XX
XX WPI; 2004-468712/44.

Query Match          92.5%; Score 546; DB 8; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.6e-38;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATITCKSSQSLYSNNKNYLGWYQKPGQPKLLIYWASTR 60
DB 21 DIVMTQSPDLSAVSLGERATITCKSSQSLYSNNKNYLAWYQKPGQPKLLIYWASTR 80
QY 61 ESGVPARFSGSGGTFTLTINSQAEDVAVYCOQYVSTPRSGGTWVEIK 113
DB 81 ESGVDRFSGSGGTFTLTISLSQAEDVAVYCOQYVSTPPMFGGQTKVEIK 133

RESULT 14
ADQ87927
ID ADQ87927 standard; protein; 135 AA.
XX
XX ADQ87927;
XX
XX 04-NOV-2004 (first entry)
XX
XX Human H5IGKAW variable light chain antibody protein.
XX
XX Primate; tolerance; antigen; mixed lymphocyte reaction; MUR; CD4+; CD25+;
XX IL-2; IL-4; IL-12; immune response; graft rejection; immunosuppressive;
XX antirheumatic; antiarthritic; antidiabetic; neuroprotective;
XX antiinflammatory; antiallergic; antiasthmatic; cytostatic; antimicrobial;
XX transplant; graft-versus-host disease; autoimmune disease; inflammation;
XX allergy; asthma; cancer; infection; human; H5IGKAW.
XX
XX Homo sapiens.
XX
XX WO2004067554-A2.
XX
XX 12-AUG-2004.
XX
XX 28-JAN-2004; 2004WO-US002643.
XX
XX 29-JAN-2003; 2003US-00353708.
XX
XX (TOLE-) TOLERRX INC.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;
XX Ringler D, Cobbold S, Winsor-Hines D;
XX
XX WPI; 2004-580970/56.
XX
XX Inducing tolerance to an antigen comprises administering a CD4 antibody
XX alone or in combination with other compounds that induce tolerance
XX against one or more antigens.
XX
```

PS Example 1; Page 30; 85pp; English.

XX The invention relates to a novel method for treating a primate to induce

CC tolerance to at least one antigen. The method comprises administering a

CC compound, or a combination of compounds, that induces tolerance against

CC one or more antigens. The compound or the combination being in a primary

CC mixed lymphocyte reaction (MLR) in vitro, which reduces the amount of

CC CD4+ CD25+ cells produced in the mixed lymphocyte reaction and that

CC generates in the primary mixed lymphocyte reaction a cell population that

CC reduces at least one of the amount of CD4+ CD25+ cells produced in vitro

CC in at least one of a primary and secondary mixed lymphocyte reactions,

CC and the amount of at least one of IL-2, IL-4 and IL-12 in a secondary

CC mixed lymphocyte reaction. The compound or the combination being

CC administered in an amount and for a time so as to induce tolerance

CC against the antigen, the compound or the combination being present in the

CC primate when the antigen is present in the primate. The invention further

CC comprises: an antibody that binds to the same epitope as the humanised

CC antibody given in the specification; a composition comprising the

CC antibody and a pharmaceutical carrier; inducing tolerance to an antigen

CC in a patient; inhibiting an immune response in a patient or for

CC inhibiting the rejection of a graft in a human patient; and screening for

CC a compound, or a combination of at least two compounds for use in

CC inducing tolerance. The compositions of the invention have the following

CC activities: immunosuppressive, antirheumatic, antiarthritic,

CC antidiabetic, neuroprotective, antiinflammatory, antiallergic,

CC antiasthmatic, cytostatic, and antimicrobial. The composition and methods

CC are useful for inhibiting, preventing or ameliorating an immune response

CC against an antigen, such as in the inhibition or treatment of transplant

CC rejection, graft-versus-host disease, autoimmune diseases (e.g.

CC rheumatoid arthritis, diabetes or multiple sclerosis), inflammation,

CC allergy, asthma, cancer or infections. These may also be used for

CC identifying compounds or agents useful for inducing tolerance against

CC antigens. This sequence represents a human HSIKAW variable light chain

XX antibody protein used in the novel method of the invention.

SQ Sequence 135 AA;

Query Match 92.5%; Score 546; DB 8; Length 135;

Best Local Similarity 92.9%; Pred. No. 1.6e-38;

Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERATITCKSSQSIYSSNNKNYLGWYQKQKPPKLLIYWASTR 60

DB 21 DIVMTQSPDSLAVSLGERATINCKSSQSIYSSNNKNYLAWYQKQKPPKLLIYWASTR 80

QY 61 ESGVPAFSGSGGTDFTLTINSIQAEDVAVYCCQYYSYTPRSPFGQGTWVEIK 113

DB 81 ESGVDRFSGSGGTDFTLTISLSIQAEDVAVYCCQYYSYTPPMFGQGTWVEIK 133

RESULT 15

ADP03811

ID ADP03811 standard; protein; 286 AA.

XX AC ADP03811;

XX DT 26-AUG-2004 (first entry)

XX DE Human antibody related protein sequence, SEQ ID 184.

XX KW Cytostatic; Antiarteriosclerotic; Antiinflammatory; Immunosuppressive;

XX KW human; antibody; cancer lesion; arteriosclerosis; inflammatory disease;

XX KW autoimmune disease; cancer.

XX OS Homo sapiens.

XX PN WO2004048571-A1.

XX PD 10-JUN-2004.

XX PF 21-NOV-2003; 2003WO-JP014919.

XX PR 22-NOV-2002; 2002JP-00339241.

XX (CHUS ) CHUGAI SEIYAKU KK.

PA (PHAR-) PHARMALOGICALS RES PTE LTD.

XX Tsuchiya M, Suzuki M, Yoshida K, Fujii E, Matsubara K, Tsunoda H;

PI WPI: 2004-450382/42.

DR N-PSDB; ADP03810.

XX Isolating polynucleotide that encodes antibody which acts against

PT lesioned tissue, involves isolating B cells that is infiltrated into

PT lesioned tissue, and acquiring polynucleotide that encodes antibody from

PT isolated B cells.

XX Example 4; SEQ ID NO 184; 200pp; Japanese.

XX The present invention relates to novel antibody sequences, which acts

CC against lesioned tissue. Also claimed is a method (M1) for isolating B

CC polynucleotide encoding the antibodies, which involves (a) isolating B

CC cells that is infiltrated into lesioned tissue, and (b) acquiring B

CC polynucleotide that encodes an antibody from the isolated B cells. The

CC antibodies are useful for treating cancer lesions, arteriosclerosis,

CC inflammatory disease or autoimmune disease. The present sequence was used

CC to illustrate the invention.

SQ Sequence 286 AA;

Query Match 92.5%; Score 546; DB 8; Length 286;

Best Local Similarity 92.0%; Pred. No. 3.4e-38;

Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERATITCKSSQSIYSSNNKNYLGWYQKQKPPKLLIYWASTR 60

DB 162 DIVMTQSPDSLAVSLGERATINCKSSQSIYSSNNKNYLAWYQKQKPPKLLIYWASTR 221

QY 61 ESGVPAFSGSGGTDFTLTINSIQAEDVAVYCCQYYSYTPRSPFGQGTWVEIK 113

DB 222 ESGVDRFSGSGGTDFTLTISLSIQAEDVAVYCCQYYSYTPPTFGQGTWVEIK 274

Search completed: November 16, 2005, 21:51:40

Job time : 66.8088 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 13.5018 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-22  
Perfect score: 590  
Sequence: 1 DIVMTQSPDLSAVSLGERAT.....COOYVSTPRSGFGTWNVEIK 113  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	91.7	113	S34002	Ig kappa chain V r
2	539	91.4	114	K4HULN	Ig kappa chain V-I
3	531	90.0	134	S49531	anti-Sm antibody V
4	530	89.8	129	S40347	Ig kappa chain - h
5	529	89.7	120	S51147	antibody light cha
6	525	89.0	113	S30520	Ig kappa chain V r
7	523	88.6	113	S34003	Ig kappa chain V r
8	522	88.5	134	K4HU17	Ig kappa chain pre
9	517	87.6	113	S30523	Ig kappa chain V r
10	514.5	87.2	133	K4HUJI	Ig kappa chain pre
11	511	86.6	114	S44116	Ig kappa chain V-J
12	508	86.1	114	S44119	Ig kappa chain V-J
13	505	85.6	121	K4HU	Ig kappa chain pre
14	505	85.6	124	S40364	Ig kappa chain - h
15	496.5	84.2	138	A53261	Ig kappa chain pre
16	495	83.9	132	S46373	Ig kappa chain V-J
17	494	83.7	101	PH0869	Ig kappa chain V r
18	487.5	82.6	106	A49138	IgA kappa rheumato
19	480.5	81.4	118	PT0356	Ig kappa chain V r
20	469	79.5	129	S40329	Ig kappa chain V-J
21	469	79.5	134	S21917	Ig kappa chain V r
22	467	79.2	136	A49137	Ig kappa chain pre
23	463	78.5	240	S06084	Ig kappa chain pre
24	461	78.1	102	A34153	Ig kappa chain V-I
25	460	78.0	134	PC1214	Ig kappa chain pre
26	460	78.0	145	PL0014	Ig kappa chain pre
27	459	77.8	113	PL0263	Ig kappa chain V r
28	457.5	77.5	112	S41393	Ig kappa chain V r
29	454	76.9	102	B34153	Ig kappa chain V-I

30	453	76.8	92	S37529	Ig kappa chain V r
31	453	76.8	113	A49260	antitumor monoclon
32	452	76.6	92	S37533	Ig kappa chain V r
33	451.5	76.5	138	S26040	Ig kappa chain pre
34	448	75.9	113	JC2270	PL7-6 antibody lig
35	447.5	75.8	112	S09970	Ig kappa chain V-J
36	447	75.8	92	S37532	Ig kappa chain V r
37	447	75.8	92	S37534	Ig kappa chain V r
38	446	75.6	92	S37535	Ig kappa chain V r
39	444	75.3	92	S37530	Ig kappa chain V r
40	444	75.3	214	S68212	Ig kappa chain (Ma
41	442.5	75.0	111	G30502	Ig kappa chain V r
42	441	74.7	112	F30538	Ig kappa chain V r
43	440	74.6	112	E30538	Ig kappa chain V r
44	440	74.6	220	A31790	Ig kappa chain V r
45	439	74.4	113	PL0264	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S34002  
IG kappa chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S34002; S30522  
R/Mariette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A/Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A/Reference number: S34001; MUID:9309281; PMID:7681398  
A/Accession: S34002  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-113 <MAR>  
A/Cross-references: EMBL:Z18328  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 541; DB 2; Length 113;  
Best Local Similarity 91.2%; Pred.No. 1.1e-41;  
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY	1	DIVMTQSPDLSAVSLGERATIIICKSSQSLYSNNKNYLGWYQKPGQPPKLIYWASTR	60
DB	1	DIVMTQSPDLSAVSLGERATINCKSSQSLYSNNKNYLGWYQKPGQPPKLIYWASTR	60
QY	61	ESGVPARFSGSGSGTDFTLTINSQAEDVAVYVYCOOYVSTPRSGFGGTWVEIK	113
DB	61	ESGVPRFSGSGSGTDFTLTISLQAEDVAVYVYCHOYVIGIPRTFGGTWVEIK	113

RESULT 2

K4HULN  
IG kappa chain V-IV region (Len) - human  
C/Species: Homo sapiens (man)  
C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 01-Dec-2000  
R/Schneider, M.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975  
A/Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette der Subgruppe IV v  
A/Reference number: A01903; MUID:76004342; PMID:50995  
A/Accession: A01903  
A/Molecule type: protein  
A/Residues: 1-114 <SCH>  
A/Note: this is the first completely sequenced V region of a new kappa chain subgroup, de  
R/Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
J. Exp. Med. 170, 1551-1558, 1989  
A/Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-asso  
A/Reference number: A61458; MUID:90039128; PMID:2478651  
A/Accession: F61458





Db 61 ESGVDPFRFSGSGGTDTLTITSSLOAEDVAVYVYCOQYNTPLTFGGGTVKEIK 113

RESULT 7

S34003

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000

C:Accession: S34003

R:Mariette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; MUID:93209281; PMID:7681398

A:Accession: S34003

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <VAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 523; DB 2; Length 113;

Best Local Similarity 89.4%; Pred. No. 4.4e-40;

Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIICKSSQSYLYSSNNKYNLYGWYQKPGQPPKLLIYWASTR 60

DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKYNLYAWYQKAGQPPKLLIYWASTR 60

QY 61 ESGVDPFRFSGSGGTDTLTITSSLOAEDVAVYVYCOQYNTPLTFGGGTVKEIK 113

DB 61 ESGVDPFRFSGSGGTDTLTITSSLOAEDVAVYVYCOQYNTPLTFGGGTVKEIK 113

RESULT 8

K4HU17

Ig kappa chain precursor V-IV region (B17) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 21-Jan-2000

C:Accession: A01905

R:Marsh, P.; Miller, F.; Gould, H.

Nucleic Acids Res. 13, 6531-6544, 1985

A:Title: Detection of a unique human V kappa IV germline gene by a cloned cDNA probe.

A:Reference number: A01905; MUID:86041854; PMID:2997713

A:Accession: A01905

A:Molecule type: mRNA

A:Residues: 1-134 <VAR>

A:Note: the sequence was determined from the differentiated gene

A:Note: the authors translated the codon TGC for residue 76 as Trp

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-134/Product: Ig kappa chain V-IV region (B17) #status predicted <MAT>

F:21-43/Region: framework 1

F:36-116/Domain: immunoglobulin homology <IMM>

F:44-60/Region: complementarity-determining 1

F:61-75/Region: framework 2

F:76-82/Region: complementarity-determining 2

F:83-114/Region: framework 3

F:115-121/Region: complementarity-determining 3

F:122-134/Region: framework 4

F:43-114/disulfide bonds: #status predicted

Query Match 88.5%; Score 522; DB 1; Length 134;

Best Local Similarity 90.3%; Pred. No. 6.4e-40;

Matches 102; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIICKSSQSYLYSSNNKYNLYGWYQKPGQPPKLLIYWASTR 60

DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKYNLYAWYQKAGQPPKLLIYWASTR 80

QY 61 ESGVDPFRFSGSGGTDTLTITSSLOAEDVAVYVYCOQYNTPLTFGGGTVKEIK 113

DB 81 ESGVDPFRFSGSGGTDTLTITSSLOAEDVAVYVYCOQYNTPLTFGGGTVKEIK 133

RESULT 9

S30523

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S30523

R:Mariette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30523

A:Molecule type: mRNA

A:Residues: 1-113 <VAR>

A:Cross-references: EMBL:Z18329

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 517; DB 2; Length 113;

Best Local Similarity 88.5%; Pred. No. 1.5e-39;

Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIICKSSQSYLYSSNNKYNLYGWYQKPGQPPKLLIYWASTR 60

DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSYLYSSNNKYNLYAWYQKAGQPPKLLIYWASTR 60

QY 61 ESGVDPFRFSGSGGTDTLTITSSLOAEDVAVYVYCOQYNTPLTFGGGTVKEIK 113

DB 61 ESGVDPFRFSGSGGTDTLTITSSLOAEDVAVYVYCOQYNTPLTFGGGTVKEIK 113

RESULT 10

K4HUJ1

Ig kappa chain precursor V-IV region (J1) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004

C:Accession: A01904

R:Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G.

Nucleic Acids Res. 13, 6515-6529, 1985

A:Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ-line gene.

A:Reference number: A93589; MUID:86041853; PMID:2997712

A:Accession: A01904

A:Molecule type: DNA

A:Residues: 1-133 <KLO>

A:Cross-references: UNIPROT:P06313; GB:Z00022; GB:X51570; NID:G33158; PIDN:CAA77317.1; P1

A:Note: the sequence was determined from the differentiated gene

C:Genetics:

A:Gene: GDB:IGKV

A:Cross-references: GDB:119341; OMIM:146980

A:Map position: 2p12-2p12

A:Introns: 17/11

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-133/Product: Ig kappa chain V-IV region (J1) #status predicted <MAT>

F:21-43/Region: framework 1

F:36-116/Domain: immunoglobulin homology <IMM>

F:44-60/Region: complementarity-determining 1

F:61-75/Region: framework 2

F:76-82/Region: complementarity-determining 2

F:83-114/Region: framework 3

F:115-122/Region: complementarity-determining 3

F:123-133/Region: framework 4

F:43-114/disulfide bonds: #status predicted

Query Match 87.2%; Score 514.5; DB 1; Length 133;

Best Local Similarity 89.4%; Pred. No. 3e-39; Mismatches 4; Indels 7; Gaps 1;  
Matches 101; Conservative

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQPGPPKLLIYWASTR 60  
|||||  
DB 21 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQPGPPKLLIYWASTR 80  
|||||  
QY 61 ESGVPRFSGSGSGTDFTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113  
|||||  
DB 81 ESGVPRFSGSGSGTDFTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 132  
|||||

## RESULT 11

S44116  
Ig kappa chain V-J region - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C/Accession: S44116  
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A/Reference number: S44105  
A/Accession: S44116  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-114 <HAW>  
A/Cross-references: EMBL:Z31391; NID:g472970; PIDN:CAA83266.1; PID:g940527  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 511; DB 2; Length 114;  
Best Local Similarity 86.7%; Pred. No. 5.2e-39; Indels 9; Gaps 0;  
Matches 98; Conservative

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQPGPPKLLIYWASTR 60  
|||||  
DB 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQPGPPKLLIYWASTR 60  
|||||  
QY 61 ESGVPRFSGSGSGTDFTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113  
|||||  
DB 61 ESGVPRFSGSGSGTDFTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113  
|||||

## RESULT 12

S44119  
Ig kappa chain V-J region - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C/Accession: S44119  
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A/Reference number: S44105  
A/Accession: S44119  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-114 <HAW>  
A/Cross-references: EMBL:Z31396; NID:g472973; PIDN:CAA83271.1; PID:g940530  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 86.1%; Score 508; DB 2; Length 114;  
Best Local Similarity 87.6%; Pred. No. 9.7e-39; Indels 11; Gaps 0;  
Matches 99; Conservative

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQPGPPKLLIYWASTR 60  
|||||  
DB 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQPGPPKLLIYWASTR 60  
|||||  
QY 61 ESGVPRFSGSGSGTDFTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113  
|||||

DB 61 ESGVPRFSGSGSGTDFTLTINSIQAEDVAVYCCQYVSTPRSGQGTWVEIK 113  
|||||

## RESULT 13

K4HU  
Ig kappa chain precursor V-IV region - human  
C/Species: Homo sapiens (man)  
C/Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
C/Accession: A01902  
R/Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G.  
Nucleic Acids Res. 13, 6515-6529, 1985  
A/Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germli  
A/Reference number: A93589; MUID:86041853; PMID:2397712  
A/Accession: A01902  
A/Molecule type: DNA  
A/Residues: 1-121 <KLO>  
A/Cross-references: UNIPROT:P06312  
A/Note: the sequence was determined from the germline gene  
A/Note: there is only one Ig kappa V-IV gene  
C/Genetics:

A/Introns: 17/1  
A/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-121/Product: Ig kappa chain precursor V-IV region #status predicted <MAT>  
F;21-43/Region: framework 1  
F;36-116/Domain: immunoglobulin homology <IMM>  
F;44-60/Region: complementarity-determining 1  
F;61-75/Region: framework 2  
F;76-82/Region: complementarity-determining 2  
F;83-114/Region: framework 3  
F;115-121/Region: complementarity-determining 3  
F;43-114/Disulfide bonds: #status predicted

Query Match 85.6%; Score 505; DB 1; Length 121;  
Best Local Similarity 95.0%; Pred. No. 1.9e-38; Indels 3; Gaps 0;  
Matches 96; Conservative

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQPGPPKLLIYWASTR 60  
|||||  
DB 21 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQPGPPKLLIYWASTR 80  
|||||

QY 61 ESGVPRFSGSGSGTDFTLTINSIQAEDVAVYCCQYVSTP 101  
|||||  
DB 81 ESGVPRFSGSGSGTDFTLTINSIQAEDVAVYCCQYVSTP 121  
|||||

## RESULT 14

S40364  
Ig kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40364  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:9408091; PMID:8258341  
A/Accession: S40364  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-124 <KLE>  
A/Cross-references: EMBL:X72474; NID:g441416; PID:g441417  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;26-106/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 505; DB 2; Length 124;  
Best Local Similarity 95.8%; Pred. No. 2e-38; Indels 11; Gaps 0;  
Matches 97; Conservative

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQPGPPKLLIYWASTR 60  
|||||

```

Db      11 DIVMTQSPDLSAVSLGERATINCKSRSLYTSNNKNYLAWYQHKFGQPPRLIIYWASNR 70
QY      61 ESGVPARFSGSGGTDFTLTINSLOAEDVAVYYCQYYSTPRSFQGGTWTWEIK 113
Db      71 ESGVPDRFASGSSTGDTFTLTISLQAEADVAVYYCQYYINPISFGGTVKQIK 123

RESULT 15
A53261
I: kappa chain precursor V-J-C region - human (fragment)
C: Species: Homo sapiens (man)
C: Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
R: Accession: A53261
J: Cogne, M.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Aucouturier, P.
A: Title: Structure of a monoclonal kappa chain of the Vk-IV subgroup in the kidney and P
A: Reference number: A53261; MUID:91250576; PMID:1904072
A: Accession: A53261
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-138 <COG>
A: Cross-references: GB:M38267
A: Note: authors translated the codon TTG for residue 12 as Phe
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin
F: 36-116/Domain: immunoglobulin homology <IMM>

Query Match      84.2%; Score 496.5; DB 2; Length 138;
Best Local Similarity 85.1%; Pred. No. 1.3e-37;
Matches 97; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY      1 DIVMTQSPDLSAVSLGERATINCKSRSLYTSNNKNYLAWYQHKFGQPPRLIIYWASTR 60
Db      21 DIVMTQSPDLSAVSLGERATINCKSLSVFFSPNNKNYLAWYQHKFGQPPRLIIYWASTR 80
QY      61 ESGVPARFSGSGGTDFTLTINSLOAEDVAVYYCQYYST-PRSFQGGTWTWEIK 113
Db      81 ESGVPDRFSGSGGTNFTLTISRQAEADVAVYYCQYYTTLSTWTFQGGTVKQIK 134
```

Search completed: November 16, 2005, 22:04:08  
Job time : 13.5018 secs

THIS PAGE BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 63.3548 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-22  
Perfect score: 590  
Sequence: 1 DIVMTQSPDSLAVSLGERAT.....COQYYSTRPSFGQGTMTVEIK 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	544	92.2	114	1	KV4A_HUMAN	P01625 homo sapien
2	535	90.7	134	1	KV4C_HUMAN	P06314 homo sapien
3	514.5	87.2	133	1	KV4B_HUMAN	P06312 homo sapien
4	505	85.6	121	1	KV4D_HUMAN	P83593 homo sapien
5	481	81.5	109	1	KV4E_HUMAN	Q6KB05 mus musculus
6	428	72.5	255	2	Q6KB05	P01605 mus musculus
7	397	67.3	108	1	KV1M_HUMAN	P01667 mus musculus
8	397	67.3	111	1	KV3Q_MOUSE	P01665 mus musculus
9	396	67.1	111	1	KV3M_MOUSE	Q9UL70
10	395	66.9	108	2	Q9UL70	P04207 homo sapien
11	394.5	66.9	129	1	KV3H_HUMAN	P01666 mus musculus
12	394	66.8	111	1	KV3N_MOUSE	P01635 homo sapien
13	393.5	66.7	129	1	KV3L_HUMAN	Q9UL79
14	393	66.6	108	2	Q9UL79	P01624 homo sapien
15	392.5	66.5	109	1	KV3F_HUMAN	P01600 homo sapien
16	391	66.3	108	1	KV1H_HUMAN	P01623 homo sapien
17	390.5	66.2	109	1	KV3E_HUMAN	P01670 mus musculus
18	390	66.1	111	1	KV3R_MOUSE	P01660 mus musculus
19	389	65.9	111	1	KV3H_MOUSE	P01669 mus musculus
20	389	65.4	108	2	KV3Q_MOUSE	Q9UL77
21	386	65.4	108	2	Q9UL77	P01620 homo sapien
22	385.5	65.3	109	1	KV3B_HUMAN	P01673 mus musculus
23	385	65.3	111	1	KV3U_MOUSE	P04431 homo sapien
24	385	65.3	129	1	KV1W_HUMAN	P06312 homo sapien
25	384	65.1	238	2	Q66J57	P01622 homo sapien
26	383.5	65.0	109	1	KV3D_HUMAN	P01664 mus musculus
27	383	64.9	111	1	KV3L_MOUSE	Q920E9 mus musculus
28	383	64.9	111	2	Q920E9	P04206 mus musculus
29	382.5	64.8	109	1	KV3G_HUMAN	P01678 homo sapien
30	382.5	64.8	109	2	Q9UL78	P18136 homo sapien
31	382.5	64.8	129	1	KV3M_HUMAN	

32	382	64.7	108	2	Q9UL83	Q9UL83 homo sapien
33	382	64.7	111	1	KV3S_MOUSE	P01671 mus musculus
34	381.5	64.7	110	1	KV3P_MOUSE	P01668 mus musculus
35	381	64.6	236	2	Q6PIT5	Q6PIT5 homo sapien
36	379.5	64.3	239	2	Q8NEK0	Q8NEK0 homo sapien
37	378.5	64.2	107	2	Q9ESA9	Q9ESA9 homo sapien
38	377	63.9	111	1	KV3J_MOUSE	P01662 mus musculus
39	376.5	63.8	109	2	Q9UL85	Q9UL85 homo sapien
40	376.5	63.8	117	1	KV2E_HUMAN	P06309 homo sapien
41	376	63.7	108	1	KV1K_HUMAN	P01603 homo sapien
42	-	376	63.7	111	KV3K_MOUSE	P01663 mus musculus
43	376	63.7	131	1	KV3I_MOUSE	P01661 mus musculus
44	375	63.6	111	1	KV3T_MOUSE	P01672 mus musculus
45	375	63.6	236	2	Q6GMW1	Q6GMW1 homo sapien

ALIGNMENTS

RESULT 1  
KV4A\_HUMAN  
ID KV4A\_HUMAN STANDARD; PRT; 114 AA.  
AC P01625;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig kappa chain V-IV region Len.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76004342; PubMed=50995;  
RA Schneider M., Hilschmann N.;  
RT "The primary structure of a monoclonic immunoglobulin-L-chain of  
subgroup IV of the kappa type (Bence-Jones protein Len).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
RN [2]  
RP REVISION TO 9.  
RA Salomon A.;  
RL Submitted (AUG-1996) to Swiss-Prot.  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
DR PDB; 1BEQ; X-ray; A/B=1-114.  
DR PDB; 1BEU; X-ray; A/B=1-114.  
DR PDB; 1ERQ; X-ray; A=1-114.  
DR PDB; 1EK3; X-ray; A/B=1-114.  
DR PDB; 1LVE; X-ray; @=1-114.  
DR PDB; 3LVE; X-ray; @=1-114.  
DR PDB; 5LVE; X-ray; A=1-114.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;  
Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 40 Complementarity-determining-1.  
FT DOMAIN 41 55 Framework-2.  
FT DOMAIN 56 62 Complementarity-determining-2.  
FT DOMAIN 63 94 Framework-3.  
FT DOMAIN 95 101 Complementarity-determining-3.  
FT DOMAIN 102 113 Framework-4.  
FT DISULFID 23 94 By similarity.  
FT STRAND 4 7  
FT STRAND 10 13  
FT STRAND 15 16  
FT STRAND 19 25



```
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Framework-3.
FT DOMAIN 115 122 Complementarity-determining-3.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 87.2%; Score 514.5; DB 1; Length 133;
Best Local Similarity 89.4%; Pred. No. 3.1e-45;
Matches 101; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 80

QY 61 ESGVPAFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 113
Db 81 ESGVPAFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGTWVEIK 132

RESULT 4
KV40_HUMAN STANDARD; PRT; 121 AA.
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-IV region precursor (fragment).
GN Name=IGKV4-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkaun G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA Zschau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -!- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00023; CAA77318.1; -
DR PIR; A01902; K4HU.
DR HSSP; P01625; 1LVE.
DR Genew; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 Ig kappa chain V-IV region.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
```

```
FT DOMAIN 83 114 Framework-3.
FT DOMAIN 115 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON_TER 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 85.6%; Score 505; DB 1; Length 121;
Best Local Similarity 95.0%; Pred. No. 2.7e-44;
Matches 96; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 80

QY 61 ESGVPAFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTP 101
Db 81 ESGVPAFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTP 121

RESULT 5
KV4D_HUMAN STANDARD; PRT; 109 AA.
AC P83593;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-IV region STH (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal adipose tissue;
RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- FUNCTION: May play an important role in fibrillogenesis.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 40 Complementarity-determining-1.
FT DOMAIN 41 55 Framework-2.
FT DOMAIN 56 62 Complementarity-determining-2.
FT DOMAIN 63 94 Framework-3.
FT DOMAIN 95 101 Complementarity-determining-3.
FT DOMAIN 102 109 Framework-4.
FT DISULFID 23 94 By similarity.
FT UNSURE 23 23
FT UNSURE 94 94
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;

Query Match 81.5%; Score 481; DB 1; Length 109;
Best Local Similarity 86.0%; Pred. No. 7.2e-42;
Matches 92; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERATITCKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db 1 DIVMTQSPDSLAVSLGERATINCRSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPAFSGSGGTDTFTLTINSLOAEDVAVYCCQYVSTPRSGGT 107
Db 61 ESGVPAFSGSGGTDTFTLTIPGLQAEDVAVYCCQYVRIPTFGG 107

RESULT 6
```

```

Q6KB05
ID Q6KB05 PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE ScFv B8E5 Protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -.
DR HSSP; P01837; INCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG-LIKE; 2.
FT NON_TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 72.5%; Score 428; DB 2; Length 255;
Best Local Similarity 73.5%; Pred. No. 5.6e-36;
Matches 83; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDSLAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKQPPKLLIYWASTR 60
Db 137 DIVMAQSPSSLVSAGEKVMSCSKSSQSLNSRNQKNYLAWYQKQKPSPKLLIYGASTR 196

Qy 61 ESGVPAFPFSGSGSDTFTLTINSLOAEDVAVYCCQYVSTPRSGFGQTWVEIK 113
Db 197 ESGVPAFPFSGSGSDTFTLTINSLOAEDVAVYCCQYVSTPRSGFGQTWVEIK 249

RESULT 7
KVIM HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IGM
anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684 (1976).
CC -1- MISCELLANEOUS: The second and third hypervariable regions of this
chain are identical with those of the human POM V-III kappa chain,
with which it shares certain idiotypic determinants.
CC -1- MISCELLANEOUS: This chain was isolated from an IGM with anti-gamma
globulin activity.
DR PIR; A01871; K1HULY.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV_v.

Query Match 67.3%; Score 397; DB 1; Length 111;
Best Local Similarity 68.1%; Pred. No. 3.5e-33;
Matches 77; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

Qy 1 DIVMTQSPDSLAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKQPPKLLIYWASTR 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVVDYDGD--SYMNWYQKQKQPPKLLIYTASNL 58

Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG-LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN 1 23 Framework-1.
DOMAIN 24 34 Framework-2.
DOMAIN 35 49 Framework-2.
DOMAIN 50 56 Complementarity-determining-1.
DOMAIN 57 88 Complementarity-determining-2.
DOMAIN 89 97 Complementarity-determining-3.
DOMAIN 98 107 Complementarity-determining-4.
DISULFID 23 88 By similarity.
NON_TER 108 108
SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 67.3%; Score 397; DB 1; Length 108;
Best Local Similarity 67.3%; Pred. No. 3.4e-33;
Matches 76; Conservative 14; Mismatches 17; Indels 6; Gaps 1;

Qy 1 DIVMTQSPDSLAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKQPPKLLIYWASTR 60
Db 1 DIVMTQSPSSLVSVDGRTVITTCQASQNV-----NAYLNWYQKQKGLAPKLLIYGASTR 54

Qy 61 ESGVPAFPFSGSGSDTFTLTINSLOAEDVAVYCCQYVSTPRSGFGQTWVEIK 113
Db 55 EAGVPSRPFSGSGSDTFTLTINSLOPEDIATYCCQYNNWPPTFGGGTKEVK 107

RESULT 8
KV3O MOUSE STANDARD; PRT; 111 AA.
ID KV3O_MOUSE
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
DR PIR; C01937; KVM508.
DR HSSP; P01665; 1QNZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN 1 23 Framework-1.
DOMAIN 24 38 Complementarity-determining-1.
DOMAIN 39 53 Framework-2.
DOMAIN 54 60 Complementarity-determining-2.
DOMAIN 61 92 Complementarity-determining-3.
DOMAIN 93 101 Complementarity-determining-4.
DOMAIN 102 111 By similarity.
DISULFID 23 92
NON_TER 111 111
SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 67.3%; Score 397; DB 1; Length 111;
Best Local Similarity 68.1%; Pred. No. 3.5e-33;
Matches 77; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

Qy 1 DIVMTQSPDSLAVSLGERATIIICKSSQSIYSSNNKNYLGWYQKQPPKLLIYWASTR 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVVDYDGD--SYMNWYQKQKQPPKLLIYTASNL 58

```



```
QY 61 ESGVPAFSGSGSGTDTLTINSLOAEDVAVYVCOQYVSTPRSGGTWVEIK 113
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 59 ESGIPARFSGSGSGTDTLTINHPVEEDAATYVCOQSNEDPFTFGSGTKLEIK 111

RESULT 9
KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01937; KVM543.
DR PDB; 1QNZ; NMR; L=1-111.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR 3D-structure; Direct protein sequencing; Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Complementarity-determining-2.
FT DOMAIN 54 60 Complementarity-determining-3.
FT DOMAIN 61 92 Complementarity-determining-4.
FT DOMAIN 93 101 Complementarity-determining-5.
FT DOMAIN 102 111 Complementarity-determining-6.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 67.1%; Score 396; DB 1; Length 111;
Best Local Similarity 68.1%; Pred.No. 4.4e-33;
Matches 77; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSYLYSSNNKYLGWYQKPGQPKLLIYWA 60
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 1 DIVLTQSPASLAVSLGRATISCKASQSYVDYDGD--SYNNWYQKPGQPKLLIYA 58

QY 61 ESGVPAFSGSGSGTDTLTINSLOAEDVAVYVCOQYVSTPRSGGTWVEIK 113
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 59 ESGIPARFSGSGSGTDTLTINHPVEEDAATYVCOQSNEDPFTFGSGTKLEIK 111

RESULT 10
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
```

```
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BDC3E41FCCA37 CRC64;

Query Match 66.9%; Score 395; DB 2; Length 108;
Best Local Similarity 68.1%; Pred.No. 5.5e-33;
Matches 77; Conservative 12; Mismatches 18; Indels 6; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSYLYSSNNKYLGWYQKPGQPKLLIYWA 60
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 1 DIQMTQSPSSLASVGRVITICRASQGI-----SNYLAWYQKPGKPKSLIYA 54

QY 61 ESGVPAFSGSGSGTDTLTINSLOAEDVAVYVCOQYVSTPRSGGTWVEIK 113
|||:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 55 QSGVPSRFSGSGSGTDTLTISLPQEDVATYVCOQYNSAPRTFGSGTKLEIK 107

RESULT 11
KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M12740; AA58992.1; -.
DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region CLL.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 54 Complementarity-determining-1.
```

```
FT DOMAIN 55 69 Framework-2.
FT DOMAIN 70 76 Complementarity-determining-2.
FT DOMAIN 77 108 Framework-3.
FT DOMAIN 109 118 Complementarity-determining-3.
FT DOMAIN 119 129 JK1 segment.
FT DISULFID 43 108 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 66.8%; Score 394.5; DB 1; Length 129;
Best Local Similarity 70.2%; Pred. No. 7.5e-33;
Matches 80; Conservative 15; Mismatches 12; Indels 7; Gaps 3;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQKQPPKLLIYWASTR 60
DB 21 EIVMTQSPATLSVSPGERATLSRASQSV---SNN---LAWYQKQKQPPRLIYGASTR 74

QY 61 ESGVPAFSGSGGTDTFTLTINSLOAEDVAVYCCQYYS-TPRSFGQGTWVEIK 113
DB 75 ATGIPARFSGSGGTFTLTISRLEDEFAVYCCQYNNWPPWTFQGTTRVEIK 128

RESULT 12
KV3N_MOUSE
ID_KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01656;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Waigert M., Gatmaian L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KWS83.
DR HSSP; P01665; IONZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
KW DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 66.8%; Score 394; DB 1; Length 111;
Best Local Similarity 67.3%; Pred. No. 7.2e-33;
Matches 76; Conservative 14; Mismatches 21; Indels 2; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQKQPPKLLIYWASTR 60
DB 1 DIVLTQSPASLAVSLGQRATISCRASQSVYDGD--SYMNWYQKQKQPPKLLIYAASNL 58

QY 61 ESGVPAFSGSGGTDTFTLTINSLOAEDVAVYCCQYYS-TPRSFGQGTWVEIK 113
DB 59 ESGIPARFSGSGGTDTFTLNHPVEEEDATYCCQSNEDPLTFGAGTKLEK 111
```

```
RESULT 13
KV3L_HUMAN
ID_KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P10022; K3HUHA.
DR HSSP; P01625; LEEQ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 55 Complementarity-determining-1.
FT DOMAIN 56 70 Framework-2.
FT DOMAIN 71 77 Complementarity-determining-2.
FT DOMAIN 78 109 Framework-3.
FT DOMAIN 110 118 Complementarity-determining-3.
FT DOMAIN 119 129 JK1 segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 66.7%; Score 393.5; DB 1; Length 129;
Best Local Similarity 65.5%; Pred. No. 9.6e-33;
Matches 74; Conservative 20; Mismatches 14; Indels 5; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLWYQKQKQPPKLLIYWASTR 60
DB 21 EIVLTQSPGTLSPGERATLSRASQSV---SSSYLAWYQKQKQPPRLIYGASSR 75

QY 61 ESGVPAFSGSGGTDTFTLTINSLOAEDVAVYCCQYYS-TPRSFGQGTWVEIK 113
DB 76 ATGIPDRFSGSGGTDTFTLTISRLEDEFAVYCCQYGTSPRTFGQGTVEIK 128

RESULT 14
Q9UL79
ID_Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```

[1]
SEQUENCE FROM N.A.
RX MEDLINE=98277133; PubMed=3614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998) .
DR DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR PIR; S30521; S30521.
DR PIR; S34090; S34090.
DR HSP; P01607; IBWV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 66.6%; Score 393; DB 2; Length 108;
Best Local Similarity 68.1%; Pred. No. 8.8e-33;
Matches 77; Conservative 11; Mismatches 19; Indels 6; Gaps 1;

Qy 1 DIVMTQSPDSLAVSLGERATIKSSQSIYSSNNKYLGMWYQKPGQPPKLLIYWASTR 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DIVMTQSPSLASTGRVITSCRMSSQI-----SSYLAWYQKPGKAPPELLIYAAS 54
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 ESVGPARPSSGSGSTDTLTINSLOAEDVAVYQYQYSPRSGQTGMVEIK 113
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 55 QSGVPSRFSGSGSTDTLTISCLQSEDFATYYQYQYSPPTFGQGTQVEIK 107
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
KV3F_HUMAN STANDARD; PRT; 109 AA.
ID KV3F_HUMAN
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region FOM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive IgM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC C-1- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01897; K3HUPM.
DR HSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23
FT NON_TER 89
FT SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 66.5%; Score 392.5; DB 1; Length 109;
Best Local Similarity 68.1%; Pred. No. 1e-32;
Matches 77; Conservative 16; Mismatches 15; Indels 5; Gaps 1;

```

THIS PAGE BLANK (CFTO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 19.2142 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357A-22

Perfect score: 590

Sequence: 1 DIVMTQSPDLSAVSLGERAT.....COQYSTRPFGQTWVEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A COMB.pep:\*
- 2: /cgn2\_6/prodata/1/iaa/5B COMB.pep:\*
- 3: /cgn2\_6/prodata/1/iaa/6A COMB.pep:\*
- 4: /cgn2\_6/prodata/1/iaa/6B COMB.pep:\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep:\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	550	93.2	113	3	US-08-525-539A-80
2	549	93.1	114	3	US-09-025-769B-17
3	549	93.1	114	4	US-09-490-070A-17
4	549	93.1	114	4	US-09-490-153-17
5	549	93.1	114	4	US-09-490-324-17
6	546	92.5	135	3	US-08-812-586-46
7	546	92.5	135	4	US-09-535-832A-43
8	544	92.2	113	4	US-09-274-163B-16
9	544	92.2	155	3	US-08-828-741B-11
10	544	92.2	155	3	US-09-160-567-11
11	544	92.2	155	4	US-09-710-299-11
12	544	92.2	155	4	US-09-509-031-11
13	544	92.2	342	3	US-08-828-741B-6
14	544	92.2	342	3	US-09-160-567-6
15	544	92.2	342	4	US-09-710-299-6
16	544	92.2	342	4	US-09-509-031-6
17	544	92.2	495	3	US-08-828-741B-4
18	544	92.2	495	3	US-09-160-567-4
19	544	92.2	495	4	US-09-710-299-4
20	544	92.2	495	4	US-09-509-031-4
21	540	91.5	114	4	US-09-274-163B-2
22	540	91.5	114	4	US-09-274-163B-6
23	539	91.4	114	1	US-08-360-125-6
24	539	91.4	114	2	US-08-450-578-6
25	539	91.4	114	2	US-09-017-628-6
26	539	91.4	114	2	US-09-014-880-6
27	539	91.4	114	4	US-08-450-363-6

28	539	91.4	114	4	US-09-274-163B-4	Sequence 4, Appli
29	539	91.4	114	4	US-09-467-903-6	Sequence 6, Appli
30	538	91.2	115	3	US-09-025-769B-31	Sequence 31, Appli
31	538	91.2	115	3	US-09-025-769B-49	Sequence 49, Appli
32	538	91.2	115	4	US-09-490-070A-31	Sequence 31, Appli
33	538	91.2	115	4	US-09-490-070A-49	Sequence 49, Appli
34	538	91.2	115	4	US-09-490-153-31	Sequence 31, Appli
35	538	91.2	115	4	US-09-490-153-49	Sequence 49, Appli
36	538	91.2	115	4	US-09-490-324-31	Sequence 31, Appli
37	538	91.2	115	4	US-09-490-324-49	Sequence 49, Appli
38	535	90.7	113	5	PCT-US93-08435-8	Sequence 8, Appli
39	532.5	90.3	141	4	US-09-582-337-16	Sequence 16, Appli
40	531	90.0	114	4	US-09-810-502-38	Sequence 38, Appli
41	530	89.8	120	1	US-08-026-320A-4	Sequence 4, Appli
42	528	89.5	133	3	US-08-463-903-4	Sequence 4, Appli
43	528	89.5	133	3	US-07-935-695-4	Sequence 4, Appli
44	528	89.5	134	4	US-08-961-309-58	Sequence 58, Appli
45	528	89.5	274	4	US-08-961-309-66	Sequence 66, Appli

ALIGNMENTS

RESULT 1

US-08-525-539A-80  
; Sequence 80, Application US/08525539A  
; Patent No. 6309636  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; APPLICANT: CERIANI, ROBERTO L.  
; APPLICANT: PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/525,539A  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DYLAN, TYLER  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 27633-20001.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-525-539A-80

Query Match 93.2%; Score 550; DB 3; Length 113;  
Best Local Similarity 92.9%; Pred. No. 3.8e-47;  
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATICKSSQSLYSNNKNYLGWYQKPPKLLIYWASTR 60  
|||||

```
Db      1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60
Qy      61 ESGVPAFSGSGSGTDFTLTINSLSQAEADVAVYYCQYYSTPRSGGQTWVEIK 113
Db      61 ESGVDPFRFGSGSGTDFTLTITSSLSQAEADVAVYYCQYYSTPTFGGQTKVEIK 113

RESULT 2
US-09-025-769B-17
; Sequence 17, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-17

Query Match      93.1%; Score 549; DB 3; Length 114;
Best Local Similarity 92.9%; Pred. No. 4.9e-47;
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60
Db      1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60
Qy      61 ESGVPAFSGSGSGTDFTLTINSLSQAEADVAVYYCQYYSTPRSGGQTWVEIK 113
Db      61 ESGVDPFRFGSGSGTDFTLTITSSLSQAEADVAVYYCQYYSTPTFGGQTKVEIK 113

RESULT 3
US-09-490-070A-17
; Sequence 17, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
```

```
;
;
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/09/490,070A
; APPLICATION NUMBER: 373
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-490-070A-17

Query Match      93.1%; Score 549; DB 4; Length 114;
Best Local Similarity 92.9%; Pred. No. 4.9e-47;
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60
Db      1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60
Qy      61 ESGVPAFSGSGSGTDFTLTINSLSQAEADVAVYYCQYYSTPRSGGQTWVEIK 113
Db      61 ESGVDPFRFGSGSGTDFTLTITSSLSQAEADVAVYYCQYYSTPTFGGQTKVEIK 113

RESULT 4
US-09-490-153-17
; Sequence 17, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
```



```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-46

Query Match          92.5%; Score 546; DB 3; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.2e-46;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQOKPGQPPKLLIYWASTR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSLIYSSNNKNYLAWSYQOKPGQPPKLLIYWASTR 80

QY 61 ESGVPAFFSGSGGTDFTLTINSLOAEDVAVYCCQYISTPRSFQGTWVEIK 113
Db 81 ESGVPAFFSGSGGTDFTLTINSLOAEDVAVYCCQYISTPRSFQGTWVEIK 133

RESULT 7
US-09-535-832A-43
; Sequence 43, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-43

Query Match          92.5%; Score 546; DB 4; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.2e-46;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQOKPGQPPKLLIYWASTR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSLIYSSNNKNYLAWSYQOKPGQPPKLLIYWASTR 80

QY 61 ESGVPAFFSGSGGTDFTLTINSLOAEDVAVYCCQYISTPRSFQGTWVEIK 113
Db 81 ESGVPAFFSGSGGTDFTLTINSLOAEDVAVYCCQYISTPRSFQGTWVEIK 133

RESULT 8
US-09-274-163E-16
; Sequence 16, Application US/09274163E
; Patent No. 6485943
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAPFEN, Rosemarie
; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 051583/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/373,380
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-274-163E-16

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-46

Query Match          92.2%; Score 544; DB 4; Length 113;
Best Local Similarity 92.0%; Pred. No. 1.5e-46;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQOKPGQPPKLLIYWASTR 60
Db 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWSYQOKPGQPPKLLIYWASTR 60

QY 61 ESGVPAFFSGSGGTDFTLTINSLOAEDVAVYCCQYISTPRSFQGTWVEIK 113
Db 61 ESGVPAFFSGSGGTDFTLTINSLOAEDVAVYCCQYISTPRSFQGTWVEIK 113

RESULT 9
US-08-828-741B-11
; Sequence 11, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sueess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-11

Query Match          92.2%; Score 544; DB 3; Length 155;
Best Local Similarity 92.0%; Pred. No. 2.2e-46;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQSIYSSNNKNYLGWYQOKPGQPPKLLIYWASTR 60
Db 30 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWSYQOKPGQPPKLLIYWASTR 89

QY 61 ESGVPAFFSGSGGTDFTLTINSLOAEDVAVYCCQYISTPRSFQGTWVEIK 113
Db 90 ESGVPAFFSGSGGTDFTLTINSLOAEDVAVYCCQYISTPRSFQGTWVEIK 142

RESULT 10
US-09-160-567-11
```



; Sequence 11, Application US/09160567  
; Patent No. 6326179  
; GENERAL INFORMATION:  
; APPLICANT: Koentgen, Frank  
; APPLICANT: Suess, Gabriele M.  
; APPLICANT: Tarlington, David M.  
; APPLICANT: Treutlein, Herbert R.  
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF  
; TITLE OF INVENTION: PRODUCING SAME  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11530

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/160,567  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/828,741  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 10591  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 155 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-160-567-11

Query Match 92.2%; Score 544; DB 3; Length 155;  
Best Local Similarity 92.0%; Pred. No. 2.2e-46;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60  
Db 30 DIVMTQSPDLSAVSLGERATINCKSSQVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 89  
QY 61 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113  
Db 90 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 142  
RESULT 11  
US-09-710-299-11  
; Sequence 11, Application US/09710299  
; Patent No. 6521741  
; GENERAL INFORMATION:  
; APPLICANT: Koentgen, Frank  
; APPLICANT: Suess, Gabriele M.  
; APPLICANT: Tarlington, David M.  
; APPLICANT: Treutlein, Herbert R.  
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF  
; TITLE OF INVENTION: PRODUCING SAME  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza

; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/710,299  
; FILING DATE: 09-NOV-6521741-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/828,741  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 10591  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 155 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-710-299-11

Query Match 92.2%; Score 544; DB 4; Length 155;  
Best Local Similarity 92.0%; Pred. No. 2.2e-46;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60  
Db 30 DIVMTQSPDLSAVSLGERATINCKSSQVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 89  
QY 61 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113  
Db 90 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 142  
RESULT 12  
US-09-509-031-11  
; Sequence 11, Application US/09509031  
; Patent No. 6590080  
; GENERAL INFORMATION:  
; APPLICANT: Koentgen, Frank  
; APPLICANT: Suess, Gabriele M.  
; APPLICANT: Tarlington, David M.  
; APPLICANT: Treutlein, Herbert R.  
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME  
; FILE REFERENCE: 13474  
; CURRENT APPLICATION NUMBER: US/09/509,031  
; CURRENT FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Kappa  
; OTHER INFORMATION: protein sequence  
US-09-509-031-11

Query Match 92.2%; Score 544; DB 4; Length 155;  
Best Local Similarity 92.0%; Pred. No. 2.2e-46;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60  
Db 30 DIVMTQSPDLSAVSLGERATINCKSSQVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 89  
QY 61 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113  
Db 90 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 142  
RESULT 12  
US-09-509-031-11  
; Sequence 11, Application US/09509031  
; Patent No. 6590080  
; GENERAL INFORMATION:  
; APPLICANT: Koentgen, Frank  
; APPLICANT: Suess, Gabriele M.  
; APPLICANT: Tarlington, David M.  
; APPLICANT: Treutlein, Herbert R.  
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME  
; FILE REFERENCE: 13474  
; CURRENT APPLICATION NUMBER: US/09/509,031  
; CURRENT FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Kappa  
; OTHER INFORMATION: protein sequence  
US-09-509-031-11

Query Match 92.2%; Score 544; DB 4; Length 155;  
Best Local Similarity 92.0%; Pred. No. 2.2e-46;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60  
Db 30 DIVMTQSPDLSAVSLGERATINCKSSQVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 89  
QY 61 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113  
Db 90 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 142  
RESULT 12  
US-09-509-031-11  
; Sequence 11, Application US/09509031  
; Patent No. 6590080  
; GENERAL INFORMATION:  
; APPLICANT: Koentgen, Frank  
; APPLICANT: Suess, Gabriele M.  
; APPLICANT: Tarlington, David M.  
; APPLICANT: Treutlein, Herbert R.  
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME  
; FILE REFERENCE: 13474  
; CURRENT APPLICATION NUMBER: US/09/509,031  
; CURRENT FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Kappa  
; OTHER INFORMATION: protein sequence  
US-09-509-031-11

Query Match 92.2%; Score 544; DB 4; Length 155;  
Best Local Similarity 92.0%; Pred. No. 2.2e-46;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIVMTQSPDLSAVSLGERATIIICKSSQILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60  
Db 30 DIVMTQSPDLSAVSLGERATINCKSSQVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 89  
QY 61 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113  
Db 90 ESGVPAFGSGSGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 142  
RESULT 12  
US-09-509-031-11  
; Sequence 11, Application US/09509031  
; Patent No. 6590080  
; GENERAL INFORMATION:  
; APPLICANT: Koentgen, Frank  
; APPLICANT: Suess, Gabriele M.  
; APPLICANT: Tarlington, David M.  
; APPLICANT: Treutlein, Herbert R.  
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME  
; FILE REFERENCE: 13474  
; CURRENT APPLICATION NUMBER: US/09/509,031  
; CURRENT FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Kappa  
; OTHER INFORMATION: protein sequence  
US-09-509-031-11

Qy	1	DIWVTQSPDLSVLGERATITICKSSQSILYSSNNKVLGYCQKPGQPKLLIYWA	60
Db	30	DIWVTQSPDLSVLGERATINCKSSQVLYSSNSKNYLAWYCQKPGQPKLLIYWA	89
Qy	61	ESGVPARFSGSGGTFTLTINSLOAEDVAVYCCQYITPSPFGQGTWVEIK	113
Db	90	ESGVPRFSGSGGTFTLTINSLOAEDVAVYCCOYITPSPFGQGTWVEIK	142

## RESULT 13

```

US-08-828-741B-6
; Sequence 6, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suesz, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-6

```

[illegible]

RESULT 14  
US-09-160-567-6  
; Sequence 6, Application US/09160567  
; Patent No. 6326179  
; GENERAL INFORMATION:  
; APPLICANT: Koentgen, Frank

```

; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-160-567-6

```

Query Match	92.2%	Score 544;	DB 3;	Length 342;
Best Local Similarity	92.0%	Fred. No. 5.3e-46;		
Matches 104; Conservative		4; Mismatches 5;	Indels 0;	Gaps 0;

  

Qy	1	DI VMTSPDSLAVSLGERATITCKSQSILYSSNNKNYLGWYQKQPQKLLIYWA	STR	60
Db	30	DI VMTSPDSLAVSLGERATINCKSQSVIYSSNNKNYLAWYQKQPQKLLIYWA	STR	89
Qy	61	ESGVPA RFSGSGSGTFTLTINSIQAEADVAVYCCQYVSTPRFGQGTWVEIK		113
Db	90	ESGVPA RFSGSGSGTFTLTINSIQAEADVAVYCCQYVSTPRFGQGTWVEIK		142

RESULT 15  
US-09-710-299-6  
; Sequence 6, Application US/09710299  
; Patent No. 6521741  
; GENERAL INFORMATION:  
; APPLICANT: Koentgen, Frank  
; Sueses, Gabriele M.  
; Tarlington, David M.  
; Treutlein, Herbert R.  
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF  
; PRODUCING SAME  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/710,299  
FILING DATE: 09-No. 6521741-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/828,741  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10591  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 342 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-710-299-6

Query Match 92.2%; Score 544; DB 4; Length 342;  
Best Local Similarity 92.0%; Pred. No. 5.3e-46;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIVMTQSPDLSAVSLGERATIICKSSQILYSSNNKNYLGWYQKFGQPPKLLIYWASTR 60  
Db |||||  
QY 30 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNYLAWYQKFGQPPKLLIYWASTR 89  
Db |||||  
QY 61 ESGVPARFSGSGGTDFTLTINSQAEDVAVYYCQYYSTPRSFQGTWVEIK 113  
Db |||||  
QY 90 ESGVPDRFSGSGGTDFTLTISQAEDVAVYYCQYYSTPYSGGTWVEIK 142  
Db |||||

Search completed: November 16, 2005, 22:07:20  
Job time : 20.2142 secs

TEMPERATURE BLANK (USPTO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 69.3787 Seconds  
(without alignments)  
681.481 Million cell updates/sec

Title: US-10-660-357A-22  
Perfect score: 590  
Sequence: 1 DIVMTQSPDLSAVSLGERAT.....COQYVSTRPFGQGTWVEIK 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	113	14	US-10-330-613-22
2	590	100.0	113	14	US-10-330-530-22
3	590	100.0	113	16	US-10-660-357-22
4	550	93.2	113	9	US-09-956-206A-80
5	550	93.2	113	18	US-10-965-616-80
6	549	93.1	122	14	US-10-010-729-51
7	548	92.9	114	17	US-10-938-353-112
8	546	92.5	135	14	US-10-171-452A-1
9	546	92.5	135	15	US-10-353-708-1
10	546	92.5	135	16	US-10-731-984-35
11	544	92.2	113	9	US-09-274-163E-16
Sequence 22, Appl					
Sequence 22, Appl					
Sequence 22, Appl					
Sequence 80, Appl					
Sequence 80, Appl					
Sequence 51, Appl					
Sequence 112, Appl					
Sequence 1, Appl					
Sequence 35, Appl					
Sequence 16, Appl					

12	544	92.2	113	18	US-10-880-028-29	Sequence 29, Appl
13	544	92.2	113	18	US-10-880-320-29	Sequence 29, Appl
14	544	92.2	114	17	US-10-700-632-70	Sequence 70, Appl
15	544	92.2	155	14	US-10-345-618-11	Sequence 11, Appl
16	544	92.2	342	14	US-10-345-618-6	Sequence 6, Appl
17	544	92.2	495	14	US-10-345-618-4	Sequence 4, Appl
18	543	92.0	179	17	US-10-644-277-140	Sequence 140, Appl
19	542	91.9	114	20	US-11-031-485-127	Sequence 127, Appl
20	541	91.7	240	9	US-09-799-514-8	Sequence 8, Appl
21	540	91.5	114	9	US-09-274-163E-2	Sequence 2, Appl
22	540	91.5	114	9	US-09-274-163E-6	Sequence 6, Appl
23	540	91.5	119	14	US-10-010-729-13	Sequence 13, Appl
24	540	91.5	264	15	US-10-264-049-4274	Sequence 4274, Ap
25	539	91.4	114	9	US-09-274-163E-4	Sequence 4, Appl
26	539	91.4	114	17	US-10-483-994-8	Sequence 8, Appl
27	539	91.4	114	18	US-10-483-993-8	Sequence 8, Appl
28	539	91.4	114	18	US-10-497-516-8	Sequence 8, Appl
29	538	91.2	114	14	US-10-125-687-11	Sequence 11, Appl
30	538	91.2	114	18	US-10-996-191-11	Sequence 11, Appl
31	535	90.7	113	17	US-10-893-576-174	Sequence 174, Appl
32	535	90.7	133	17	US-10-893-576-26	Sequence 26, Appl
33	534	90.5	113	17	US-10-893-576-173	Sequence 173, Appl
34	534	90.5	133	17	US-10-893-576-36	Sequence 36, Appl
35	533	90.3	163	17	US-10-644-277-100	Sequence 100, Appl
36	533	90.3	220	17	US-10-644-277-20	Sequence 20, Appl
37	532.5	90.3	141	14	US-10-390-986-16	Sequence 16, Appl
38	531	90.0	114	9	US-09-810-502-38	Sequence 38, Appl
39	531	90.0	114	16	US-10-884-133-38	Sequence 108, Appl
40	531	90.0	149	17	US-10-644-277-108	Sequence 112, Appl
41	531	90.0	159	17	US-10-644-277-112	Sequence 88, Appl
42	530	89.8	115	18	US-10-734-661A-88	Sequence 12, Appl
43	530	89.8	163	17	US-10-644-277-12	Sequence 4266, Ap
44	530	89.8	211	15	US-10-264-049-4266	Sequence 136, Appl
45	529	89.7	173	17	US-10-644-277-136	

ALIGNMENTS

RESULT 1  
US-10-330-613-22  
; Sequence 22, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ARGENIX 022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-22

Query Match 100.0%; Score 590; DB 14; Length 113;  
Best Local Similarity 100.0%; Pred. No. 1.9e-45;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIVMTQSPDLSAVSLGERATII	CKSQSYLYSSNNKNYLGWYQOKPQPPKLIYWASTR	60
Db	1	DIVMTQSPDLSAVSLGERATII	CKSQSYLYSSNNKNYLGWYQOKPQPPKLIYWASTR	60
QY	61	ESGVPARFSGSGGTDFTLTIN	SLQAEADVAVYVYCCQYVSTRPFRFGQGTWVEIK	113
Db	61	ESGVPARFSGSGGTDFTLTIN	SLQAEADVAVYVYCCQYVSTRPFRFGQGTWVEIK	113

RESULT 2

```
US-10-330-530-22
; Sequence 22, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-22

Query Match      100.0%; Score 590; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DIVMTQSPDLSAVSLGERATIIICKSSQSIILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db      1 DIVMTQSPDLSAVSLGERATIIICKSSQSIILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60

Qy      61 ESGVPAFSGSGGTDFTLTINSLSQAEADVAVYCCQYVSTPRSGGTWVEIK 113
Db      61 ESGVPAFSGSGGTDFTLTINSLSQAEADVAVYCCQYVSTPRSGGTWVEIK 113

RESULT 3
US-10-660-357-22
; Sequence 22, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-22

Query Match      100.0%; Score 590; DB 16; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DIVMTQSPDLSAVSLGERATIIICKSSQSIILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db      1 DIVMTQSPDLSAVSLGERATIIICKSSQSIILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60

Qy      61 ESGVPAFSGSGGTDFTLTINSLSQAEADVAVYCCQYVSTPRSGGTWVEIK 113
Db      61 ESGVPAFSGSGGTDFTLTINSLSQAEADVAVYCCQYVSTPRSGGTWVEIK 113

RESULT 4
US-09-956-206A-80
; Sequence 80, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MUC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81

US-10-330-530-22
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MUC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-956-206A-80

Query Match      93.2%; Score 550; DB 9; Length 113;
Best Local Similarity 92.9%; Pred. No. 7.4e-42;
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DIVMTQSPDLSAVSLGERATIIICKSSQSIILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
Db      1 DIVMTQSPDLSAVSLGERATIIICKSSQSIILYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60

Qy      61 ESGVPAFSGSGGTDFTLTINSLSQAEADVAVYCCQYVSTPRSGGTWVEIK 113
Db      61 ESGVPAFSGSGGTDFTLTINSLSQAEADVAVYCCQYVSTPRSGGTWVEIK 113

RESULT 5
US-10-965-616-80
; Sequence 80, Application US/10965616
; Publication No. US20050169915A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MUC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/965,616  
FILING DATE: 13-Oct-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,206  
FILING DATE: 17-Sep-2001  
APPLICATION NUMBER: US 08/525,539  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/US95/11683  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: 08/487,598  
FILING DATE: 7-JUNE-1995  
APPLICATION NUMBER: 08/307,868  
FILING DATE: 16-SEPT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WITT, ERIC  
REGISTRATION NUMBER: 44,408  
REFERENCE/DOCKET NUMBER: 276332000101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 80:  
US-10-965-616-80  
Query Match 93.2%; Score 550; DB 18; Length 113;  
Best Local Similarity 92.9%; Pred. No. 7.4e-42;  
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIVMTQSPDSLAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60  
DB 1 DIVMTQSPDSLAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60  
QY 61 ESGVPAFSGSGGTDFTLTINSQAEDVAVYCCQYYSTPRSFQGGTWEIK 113  
DB 61 ESGVDPFRFSGSGGTDFTLTISLQAEDVAVYCCQYYSTPTFTFGGQTKVEIK 113  
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous System  
FILE REFERENCE: 1199-1-005CIP2  
CURRENT APPLICATION NUMBER: US/10/010,729  
CURRENT FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: 09/730,473  
PRIOR FILING DATE: 2000-12-05

PRIOR APPLICATION NUMBER: 09/580,787  
PRIOR FILING DATE: 2000-05-30  
PRIOR APPLICATION NUMBER: 09/322,862  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 08/779,784  
PRIOR FILING DATE: 1997-01-07  
PRIOR APPLICATION NUMBER: 08/692,084  
PRIOR FILING DATE: 1996-08-08  
PRIOR APPLICATION NUMBER: 08/236,520  
PRIOR FILING DATE: 1994-04-29  
NUMBER OF SEQ ID NOS: 80  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 51  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-010-729-51  
Query Match 93.1%; Score 549; DB 14; Length 122;  
Best Local Similarity 92.0%; Pred. No. 9.9e-42;  
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DIVMTQSPDSLAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60  
DB 1 DIVMTQSPDSLAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60  
QY 61 ESGVPAFSGSGGTDFTLTINSQAEDVAVYCCQYYSTPRSFQGGTWEIK 113  
DB 61 ESGVDPFRFSGSGGTDFTLTISLQAEDVAVYCCQYYSTPTFTFGGQTKVEIK 113  
RESULT 7  
US-10-938-353-112  
Sequence 112, Application US/10938353  
Publication No. US20050059113A1  
GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: DEVALARAJA, MADHAV NARASIMHA  
APPLICANT: FOLTZ, IAN  
APPLICANT: HAAK-FRENDSCHO, MARY  
APPLICANT: KELLERMANN, SIRID-AIMEE  
APPLICANT: LOW, JOSEPH EDWIN  
APPLICANT: MOBLEY, JAMES LESLIE  
TITLE OF INVENTION: ANTIBODIES TO M-CSF  
FILE REFERENCE: ABX-PP4  
CURRENT APPLICATION NUMBER: US/10/938,353  
CURRENT FILING DATE: 2004-09-09  
PRIOR APPLICATION NUMBER: 60/502,163  
PRIOR FILING DATE: 2003-09-10  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 112  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-938-353-112  
Query Match 92.9%; Score 548; DB 17; Length 114;  
Best Local Similarity 92.9%; Pred. No. 1.1e-41;  
Matches 105; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIVMTQSPDSLAVSLGERATIIICKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60  
DB 1 DIVMTQSPDSLAVSLGERATINCKSSQSYLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 60  
QY 61 ESGVPAFSGSGGTDFTLTINSQAEDVAVYCCQYYSTPRSFQGGTWEIK 113  
DB 61 ESGVDPFRFSGSGGTDFTLTISLQAEDVAVYCCQYYSTPTFTFGGQTKVEIK 113  
RESULT 8  
US-10-171-452A-1  
Sequence 1, Application US/10171452A

```
; Publication No. US20030108518A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
; FILE REFERENCE: 695458-59
; CURRENT APPLICATION NUMBER: US/10/171,452A
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 1
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-452A-1

Query Match          92.5%; Score 546; DB 14; Length 135;
Best Local Similarity 92.9%; Pred. No. 2e-41;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDSLAVSLGERATICKSSQSIYSSNNKNYLGMWYQKPGQPKLLIYWASTR 60
Db 21 DIVMTQSPDSLAVSLGERATICKSSQSIYSSNNKNYLGMWYQKPGQPKLLIYWASTR 80

Qy 61 ESGVPRFSGSGSDTFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 113
Db 81 ESGVPRFSGSGSDTFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 133

RESULT 9
US-10-353-708-1
; Sequence 1, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
```

```
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 1
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-353-708-1

Query Match          92.5%; Score 546; DB 15; Length 135;
Best Local Similarity 92.9%; Pred. No. 2e-41;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDSLAVSLGERATICKSSQSIYSSNNKNYLGMWYQKPGQPKLLIYWASTR 60
Db 21 DIVMTQSPDSLAVSLGERATICKSSQSIYSSNNKNYLGMWYQKPGQPKLLIYWASTR 80

Qy 61 ESGVPRFSGSGSDTFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 113
Db 81 ESGVPRFSGSGSDTFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 133

RESULT 10
US-10-731-984-35
; Sequence 35, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-731-984-35

Query Match          92.5%; Score 546; DB 16; Length 135;
Best Local Similarity 92.9%; Pred. No. 2e-41;
Matches 105; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDSLAVSLGERATICKSSQSIYSSNNKNYLGMWYQKPGQPKLLIYWASTR 60
Db 21 DIVMTQSPDSLAVSLGERATICKSSQSIYSSNNKNYLGMWYQKPGQPKLLIYWASTR 80

Qy 61 ESGVPRFSGSGSDTFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 113
Db 81 ESGVPRFSGSGSDTFTLTINSIQAEADVAVYCCQYVSTPRSGQGTWVEIK 133

RESULT 11
US-09-274-163E-16
; Sequence 16, Application US/09274163E
; Patent No. US20020137897A1
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIEFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 051583/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/373,380
```



```
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-274-163E-16

Query Match          92.2%; Score 544; DB 9; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTISLQAEADVAVYCCQYYSTPYSPFGQGTKEIK 113

RESULT 12
US-10-880-028-29
; Sequence 29, Application US/10880028
; Publication No. US20050163782A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tzung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,028
; PRIOR FILING DATE: 2004-06-28
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2003-10-03
; PRIOR FILING DATE: 2003-10-28
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-028-29

Query Match          92.2%; Score 544; DB 18; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTISLQAEADVAVYCCQYYSTPYSPFGQGTKEIK 113

RESULT 13
US-10-880-320-29
; Sequence 29, Application US/10880320
; Publication No. US20050163783A1
; GENERAL INFORMATION:
```

```
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tzung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,320
; PRIOR FILING DATE: 2004-06-28
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2003-10-03
; PRIOR FILING DATE: 2003-10-28
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-320-29

Query Match          92.2%; Score 544; DB 18; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTISLQAEADVAVYCCQYYSTPYSPFGQGTKEIK 113

RESULT 14
US-10-700-632-70
; Sequence 70, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-70

Query Match          92.2%; Score 544; DB 17; Length 114;
Best Local Similarity 92.0%; Pred. No. 2.6e-41;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERATIIKSSQSYLYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWYQKPGQPPKLLIYWASTR 60

QY 61 ESGVPARFSGSGGTDTLTINSLOAEDVAVYCCQYYSTPRSFQGTWVEIK 113
DB 61 ESGVPRFSGSGGTDTLTISLQAEADVAVYCCQYYSTPYSPFGQGTKEIK 113
```

RESULT 15  
US-10-345-618-11  
; Sequence 11, Application US/10345618  
; Publication No. US20030148484A1  
; GENERAL INFORMATION:  
; APPLICANT: Koentgen, Frank  
; APPLICANT: Suess, Gabriele M.  
; APPLICANT: Tarlinton, David M.  
; APPLICANT: Treutlein, Herbert R.  
; TITLE OF INVENTION: CATALYTIC ANTIBOIDS AND A METHOD OF PRODUCING SAME  
; FILE REFERENCE: 13474  
; CURRENT APPLICATION NUMBER: US/10/345,618  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US/09/509,031  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Kappa  
; OTHER INFORMATION: protein sequence  
US-10-345-618-11

Query Match 92.2%; Score 544; DB 14; Length 155;  
Best Local Similarity 92.0%; Pred. No. 3.5e-41;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 1 DIVMTSPDSLAVSLGERATIIICKSQSIIYSSNNKNYLGWYQKPGQPPKLLIYWASTR 60  
Db 30 DIVMTSPDSLAVSLGERATINCKSQSIIYSSNNKNYLGWYQKPGQPPKLLIYWASTR 89  
  
Qy 61 ESGVPAFFSGSGGTDFTLTINSIQAEDVAVYYCQYYSTPSFGQGTWVEIK 113  
Db 90 ESGVPAFFSGSGGTDFTLTINSIQAEDVAVYYCQYYSTPSFGQGTWVEIK 142

Search completed: November 16, 2005, 23:05:43  
Job time : 70.3787 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-26  
Perfect score: 562  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQQYDTLPLTGGTKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003Bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	562	100.0	107	7	Adc99797 Anti-huma
2	562	100.0	107	7	Adc05401 Anti-MUC1
3	562	100.0	107	7	Adf09839 Human ant
4	530	94.3	107	8	Adp22412 Human ant
5	527	93.8	108	4	Aau02534 Anti-adip
6	525	93.4	107	2	Aar54319 Anti-HIV
7	525	93.4	107	2	Aaw01287 VL region
8	525	93.4	107	3	Aay98248 Anti-gp12
9	525	93.4	107	3	Aay95139 Anti-gp12
10	523.5	93.1	241	2	Aay21892 Amino aci
11	523	93.1	113	7	Adp28271 Human het
12	523	93.1	152	8	Adk52350 Human het
13	523	93.1	164	7	Adp28243 Human het
14	521	92.7	502	8	Adn97515 Artificial
15	518	92.2	236	7	Adp93785 Monoclon
16	515	91.6	214	8	Adk523358 Human het
17	511	90.9	113	7	Adp28275 Human het
18	511	90.9	164	7	Adp28246 Human het
19	509.5	90.7	238	2	Aay21880 Amino aci
20	506	90.0	107	2	Aaw87455 Humanised
21	505	89.9	272	8	Ado19054 Human ant
22	502	89.3	107	2	Aar54262 Anti-HIV
23	502	89.3	107	2	Aaw01286 VL region
24	502	89.3	107	3	Aay98247 Anti-gp12
25	502	89.3	107	3	Aay95138 Anti-gp12

26	498	88.6	108	4	AAB62785	Aab62785 Human HIV
27	496.5	88.3	106	8	ADP22244	Adp22244 Human ant
28	496	88.3	139	7	ADP90904	Adp90904 Human hep
29	495	88.1	108	8	ADO60452	Ado60452 Human REI
30	494	87.9	108	6	ABO10817	Abol0817 Human ger
31	493	87.7	108	8	ADN41877	Adn41877 Humanised
32	491	87.4	260	5	ABP41164	Abp41164 Human ova
33	487	86.7	107	8	ADR40423	Adr40423 Reshaped
34	487	86.7	107	8	ADR40341	Adr40341 Reshaped
35	487	86.7	120	4	ABG11908	Abg11908 Novel hum
36	486	86.5	107	2	AAR81329	Aar81329 Human REI
37	486	86.5	107	2	AAW86804	Aaw86804 Variable
38	486	86.5	107	2	AAW70623	Aaw70623 Humanised
39	486	86.5	107	2	AAW42275	Aay42275 Human REI
40	486	86.5	107	5	AAU78328	Aau78328 Human REI
41	486	86.5	107	5	ABP61192	Abp61192 Humanised
42	486	86.5	107	6	ABU09373	Abu09373 Light cha
43	486	86.5	107	6	ABU10148	Abu10148 Human REI
44	486	86.5	107	6	ABU62765	Abu62765 Light cha
45	486	86.5	107	7	AAE39071	Aae39071 REI VL pr

ALIGNMENTS

RESULT 1  
ADC99797  
ID ADC99797 standard; protein; 107 AA.  
XX  
AC ADC99797;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 26.  
XX  
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; Colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057838-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041581.  
XX  
PR 28-DEC-2001; 2001US-0346299P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
DR WPI; 2003-587113/55.  
DR N-PSDB; ADC99799.  
XX  
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.  
XX  
PS Claim 3; SEQ ID NO 26; 78pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody

```
CC light chain protein of the invention.
XX
SQ Sequence 107 AA;
  Query Match      100.0%; Score 562; DB 7; Length 107;
  Best Local Similarity 100.0%; Pred. No. 2.1e-34;
  Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60

QY 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107

RESULT 2
ADF05401
ID ADD05401 standard; protein; 107 AA.
XX
AC ADD05401;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID NO 26.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
XX
DR N-PSDB; ADD05403.
XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 3; SEQ ID NO 26; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
SQ Sequence 107 AA;
  Query Match      100.0%; Score 562; DB 7; Length 107;
  Best Local Similarity 100.0%; Pred. No. 2.1e-34;
  Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60

QY 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107

RESULT 3
ADF09839
ID ADF09839 standard; protein; 107 AA.
XX
AC ADF09839;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #7.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-598367/56.
XX
DR N-PSDB; ADF09841.
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumour
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 3; SEQ ID NO 26; 83pp; English.
XX
CC The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 107 AA;
  Query Match      100.0%; Score 562; DB 7; Length 107;
  Best Local Similarity 100.0%; Pred. No. 2.1e-34;
  Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCOASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60

QY 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107
Db 61 RFSGSGSGTDFTTISGLQPEDIAITYCQYDTLPLTFGGGTKVEIK 107
```

RESULT 4  
ADP22412  
ID ADP22412 standard; protein; 107 AA.  
AC ADP22412;  
XX  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human anti-TNFa antibody light chain variable region SEQ ID NO:318.  
DE  
DE human: monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;  
KW antibacterial; antiinflammatory; antipsoaric; antirheumatic;  
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
KW prostate cancer; immuno-mediated inflammatory disease;  
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KW septic shock; cachexia; anorexia; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
XX WO2004050683-A2.  
XX  
XX 17-JUN-2004.  
XX  
XX 02-DEC-2003; 2003WO-US038281.  
XX  
XX 02-DEC-2002; 2002US-0430729P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Babcock JS, Kang JS, Foord O, Green L, Peng X, Klakamp S;  
PI Haak-Frendscho M, Rathnasami P, Pigott C, Liang ML, Lee R;  
PI Manchulenchu K, Faggioni R, Senaldi G, Qiaojuan JS;  
XX  
XX WPI; 2004-480601/45.  
XX  
XX New recombinant human monoclonal antibody that specifically binds to  
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
PT arthritis.  
XX  
XX Example 10; SEQ ID NO 318; 213pp; English.  
XX  
XX The present invention describes a human monoclonal antibody (I) that  
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
CC (M1) the level of TNFa in a patient sample, comprising contacting with  
CC (I), and detecting the level of binding between the antibody and TNFa in  
CC the sample; (2) a composition comprising the antibody or its functional  
CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
CC animal in need of treatment for the disease by administering the human  
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
CC apoptosis in an animal by selecting an animal in need of treatment for  
CC TNFa induced apoptosis by administering the human monoclonal antibody of  
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
CC antibacterial, antiinflammatory, antipsoaric, antirheumatic, eating-  
CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,

CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
CC diseases such as rheumatoid arthritis, glomerulonephritis, Crohn's  
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
CC multiple sclerosis. The present sequence represents a human anti-TNFa  
CC antibody light chain variable region, which is used in the  
CC exemplification of the present invention.  
XX  
XX  
SQ Sequence 107 AA;  
Query Match 94.3%; Score 530; DB 8; Length 107;  
Best Local Similarity 93.5%; Pred. No. 4.9e-32;  
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTITCQASQDINNNYNNYQKPGKAPKLLIYDASNLETVGPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCQASQDINNNYNNYQKPGKAPKLLIYDASNLETVGPS 60  
QY 61 RFSGSGSGTDFTFTISGLPEDIATYYCOQYDTLPLTGGGTVKVEIK 107  
DB 61 RFSGSGSGTDFTFTISGLPEDIATYYCOQYDTLPLTGGGTVKVEIK 107  
RESULT 5  
AAU02534  
ID AAU02534 standard; protein; 108 AA.  
XX  
XX AC AAU02534;  
XX  
XX DT 29-AUG-2001 (first entry)  
XX  
XX DE Anti-adipocyte monoclonal antibody light chain, FAT 22.  
XX  
XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;  
KW heart disease; complementarity determining region; CDR.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200127279-A1.  
XX  
XX PD 19-APR-2001.  
XX  
XX PF 11-OCT-2000; 2000WO-GB003900.  
XX  
XX PR 12-OCT-1999; 99US-0158812P.  
XX  
XX PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX PI Edwards BM, Main SH, Vaughan TJ;  
XX  
XX DR WPI; 2001-282031/29.  
XX  
XX N-PSDB; AAS03434.  
XX  
XX PT Panel of specific binding members of antibody molecules which bind to  
XX whole adipocytes is used in the treatment of obesity and obesity related  
XX diseases.  
XX  
XX PS Claim 1; Page 113-114; 182pp; English.  
XX  
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid  
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,  
XX and heavy chain complementarity determining regions (CDR) of the  
XX invention. The antibodies can be used in the treatment of obesity and  
XX obesity related diseases. The antibodies can be used to deliver drugs or  
XX pro-drugs directly to the fat mass of an obese patient or the antibody  
XX can be used as a therapeutic itself. Antibodies binding specifically to  
XX adipocytes can be used to activate the immune system to destroy the cells  
XX by complement mediated lysis. The antibodies may be labeled with a  
XX detectable label such as radiolabel, fluorescent or chemical group and  
XX used in methods of diagnosis in human subjects e.g. to determine the  
XX presence of adipocyte antigen on the surface of an adipocyte to detect or  
XX determine the presence or level of adipocytes in a cell or tissue sample.  
XX The antibodies can be used as an alternative means of treatment for obese

CC patients other than undergoing surgery to remove excess fat. Antibodies  
CC for different types of fat deposits can also be produced e.g. intra-  
CC abdominal fat associated with heart disease  
XX  
SQ Sequence 108 AA;  
Query Match 93.8%; Score 527; DB 4; Length 108;  
Best Local Similarity 92.5%; Pred. No. 8.3e-32;  
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DIQQTSPSSLSASVGDRTVITTCQASQDINNLYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
DB 1 DIQLTQSPSSLSASVGDRTVITTCQASQDISNLYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGKVEIK 107  
DB 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDNLPLTFGGGTRLEIK 107  
RESULT 6  
AAR54319  
ID AAR54319 standard; protein; 107 AA.  
XX  
AC AAR54319;  
XX  
AC AC  
XX  
DT 25-MAR-2003 (revised)  
DT 10-NOV-1994 (first entry)  
XX  
XX Anti-HIV gp120 immunoglobulin light chain variable region B26.  
XX  
DE Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
KW neutralisation; monoclonal antibody; kappa light chain; variable region;  
KW framework; complementarity determining region.  
XX  
XX Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 1..21  
FT /label= FR1  
FT Region 22..33  
FT /label= CDR1  
FT Region 34..48  
FT /label= FR2  
FT Region 49..55  
FT /label= CDR2  
FT Region 56..87  
FT /label= FR3  
FT Region 88..95  
FT /label= CDR3  
FT Region 96..107  
FT /label= FR4  
XX  
XX WO9407922-A1.  
XX  
XX 14-APR-1994.  
XX  
XX 30-SEP-1993; 93WO-US009328.  
XX  
XX 30-SEP-1992; 92US-00954148.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Burton DR, Barbas CF, Lerner RA;  
XX WPI; 1994-135516/16.  
XX  
XX New human monoclonal antibodies neutralising HIV - react with gp120 or  
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro  
PT diagnosis and for passive immuno-therapy.  
XX  
XX Example; Page 192; 248pp; English.  
XX  
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification

CC using primers specific for heavy and light chain variable regions. The  
CC amplification products were inserted into a dicistronic vector to produce  
CC a library of fragments. E.coli XLI Blue cells were transformed with the  
CC library. Filamentous phage were produced which expressed the MAb regions  
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of  
CC immunoreactive clones. The light chain VK region sequence AAR54319  
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 107 AA;  
Query Match 93.4%; Score 525; DB 2; Length 107;  
Best Local Similarity 94.3%; Pred. No. 1.2e-31;  
Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 3 QMTQSPSSLSASVGDRTVITTCQASQDINNLYLNWYQKPGKAPKLLIYDASNLETGVPSRF 62  
DB 1 EUTQSPSSLSASVGDRTVITTCQASQDISNHLNMYQKPGKAPKLLIYDASNLETGVPSRF 60  
QY 63 SGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGKVEIK 107  
DB 61 SGSGSGTDFTTISGLQPEDIATYCCQYDNLPLTFGGGKVEIK 105  
RESULT 7  
AAR54319  
ID AAR54319 standard; protein; 107 AA.  
XX  
AC AAR54319;  
XX  
DT 29-JAN-1997 (first entry)  
XX  
XX VL region of HIV neutralising MAb, clone B26.  
XX  
DE Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;  
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
KW virus infectivity assay; precursor gp160; immunocompetence; human;  
KW anti-HIV antibody; detection; HIV infection.  
XX  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..21  
FT /label= FR1  
FT Region 22..32  
FT /label= CDR1  
FT Region 33..47  
FT /label= FR2  
FT Region 48..54  
FT /label= CDR2  
FT Region 55..86  
FT /label= FR3  
FT Region 87..95  
FT /label= CDR3  
FT Region 96..107  
FT /label= FR4  
XX  
XX WO9602273-A1.  
XX  
XX 01-FEB-1996.  
XX  
XX 11-JUL-1995; 95WO-US008743.  
XX  
XX 18-JUL-1994; 94US-00276852.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Burton DR, Barbas CF, Lerner RA;  
XX WPI; 1996-179601/18.  
XX  
XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive  
PT immuno:therapy and detection of HIV infection.  
XX

[illegible]

XX The present sequence represents a fragment of an anti-human  
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV  
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an  
CC in vitro virus infectivity assay by 50%, at a concentration of less than  
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and  
CC immunotherapy of HIV induced diseases. They are useful as neutralising  
CC field isolates and provide useful information regarding the  
CC immunocompetence of an immune response in HIV infected patients. The  
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies  
CC which can be used to screen human monoclonal antibodies to identify  
CC whether the antibody has the same binding specificity as the antibodies  
CC of the invention. The neutralising antibodies define new epitopes on the  
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new  
CC immunotherapeutic human monoclonal antibodies. A major advantage of the  
CC monoclonal antibodies derives from the fact that they are encoded by a  
CC human polynucleotide sequence. Thus in vivo use of the monoclonal  
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly  
CC reduces the problems of significant host immune response to the passively  
CC administered antibodies which is a problem commonly encountered when  
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.  
CC An additional major advantage of the monoclonal antibodies described  
CC derives from the fact that they immunoreact with a unique determinant  
CC present on mature HIV glycoprotein gp120. This class of antibodies is  
CC particularly effective at neutralising field isolates of HIV  
XX  
SQ Sequence 107 AA;

Query Match 93.4%; Score 525; DB 3; Length 107;  
Best Local Similarity 94.3%; Pred. No. 1.2e-31;  
Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
Qy 3 QMTQSPSSLSASVGDRTITTCQASQDINNNLWYQKPGKAPKLLIYDASNLETGVSRRF 62  
Db 1 ELTQSPSSLSASVGDRTITTCQASQDINNNLWYQKPGKAPKLLIYDASNLETGVSRRF 60  
Qy 63 SGSGSGTDFTTTISGLQPEDIATYYCQYDPLPTFGGGTKVEIK 107  
Db 61 SGSGSGTDFTTTISGLQPEDIATYYCQYDNLPLTFGGGTKVEIK 105

RESULT 10  
AAY21882  
ID AAY21882 standard; protein; 241 AA.  
XX AC AAY21882;  
XX DT 24-SEP-1999 (first entry)  
XX DX Amino acid sequence of antibody ITA7.  
DE DE  
XX KW Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody;  
KW diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy; ITA7.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Misc-difference 102 /label= unknown  
FT /note= "encoded by NAG"  
XX EP934953-A2.  
XX 11-AUG-1999.  
XX 01-DEC-1998; 98EP-00122546.  
XX 03-DEC-1997; 97US-0067428P.  
XX (BOEF ) BOEHRINGER MANNHEIM CORP.

PI Winter GP, Mahoney W, Sawyer JR;  
XX WPI; 1999-432068/37.  
DR N-PSDB; AAX86938.  
XX PT New anti-complex antibody useful for diagnosing prostate cancer.  
XX PS Claim 27; Page 23-24; 42pp; English.  
XX CC The invention relates to an antibody that binds a complex between  
CC prostate-specific antigen (PSA) and anti-chymotrypsin (ACT), and has an  
CC affinity for the complex which is at least 10 fold higher than the  
CC affinity for either PSA or ACT alone. The antibody is used in diagnostic  
CC assays to detect PSA-ACT in serum samples from patients. The levels of  
CC PSA-ACT complex increase in patients suffering from prostate cancer  
CC compared to the levels in patients with benign or no growths in the  
CC prostate. Therefore detection of PSA in complex with ACT is useful for  
CC the early detection of prostate tumours, by distinguishing between benign  
CC and malignant conditions of the prostate as well as for the management of  
CC patients with prostate cancer, such as the disclosure of metastasis and  
CC the monitoring of the PSA levels after treatment. The antibodies may also  
CC be used in immunotherapy, affinity chromatography and isolation or  
CC purification of PSA-ACT. Unlike prior art antibodies which bind to PSA-  
CC ACT complexes but may also bind PSA or ACT alone, the present antibody is  
CC specific for PSA-ACT alone. Diagnostic assays using the antibodies are  
CC more accurate in diagnosing prostate cancer as they only detect the  
CC intact complex of PSA-ACT. Sequences AAY21880-884 represent specific  
CC examples of antibodies directed against PSA-ACT. The present sequence  
CC represents the amino acid sequence of antibody ITA7  
XX  
SQ Sequence 241 AA;

Query Match 93.1%; Score 523.5; DB 2; Length 241;  
Best Local Similarity 95.3%; Pred. No. 3.1e-31;  
Matches 102; Conservative 1; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 DIQMTQSPSSLSASVGDRTITTCQASQDINNNLWYQKPGKAPKLLIYDASNLETGVS 60  
Db 135 DIQMTQSPSSLSASVGDRTITTCQASQDINNNLWYQKPGKAPKLLIYDASNLETGVS 194  
Qy 61 RFSGSGSGTDFTTISGLQPEDIATYYCQYDPLPTFGGGTKVEIK 107  
Db 195 RFSGSGSGTDFTTISGLQPEDIATYYCQYDNLPLTFGGGTKVEIK 240

RESULT 11  
ADD28271  
ID ADD28271 standard; protein; 113 AA.  
XX AC ADD28271;  
XX DT 15-JAN-2004 (first entry)  
XX DX Human heterodimeric antibody light chain kappa region SEQ ID NO:49.  
DE DE  
XX KW human heterodimeric antibody; human; antibody; binding affinity;  
KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;  
KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;  
KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;  
KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.  
XX OS Synthetic.  
XX OS Homo sapiens.  
XX WO2003076568-A2.  
XX 18-SEP-2003.  
XX 11-FEB-2003; 2003WO-US004206.  
XX 11-FEB-2002; 2002US-0356086P.  
XX 29-APR-2002; 2002US-0376408P.  
XX 27-SEP-2002; 2002US-0414053P.



```

PR 25-NOV-2002; 2002US-0428807P.
XX (ALEX-) ALEXION PHARM INC.
XX Bowdish KS, Wild MA;
XX WPI; 2003-722327/68.
XX New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX Claim 9; SEQ ID NO 49; 67pp; English.
XX The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10-8 M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody light chain
CC kappa region amino acid sequence, which is used in the exemplification of
CC the present invention.
XX Sequence 113 AA;
XX
Query Match 93.1%; Score 523; DB 7; Length 113;
Best Local Similarity 93.5%; Pred. No. 1.7e-31;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
Db 3 DIQMTQSPSSLSASVGRVTITTCQASQDINNNYLNWYQKPGKAPKLLIYDASNLETVGPS 62
QY 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
Db 63 RFGSGSGDTFTTISGLQPEDIATYCCQYDNLGVTFGGTKVDIK 109
XX
RESULT 12
ADK52350
ID ADK52350 standard; protein; 152 AA.
XX
AC ADK52350;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #14.
XX
KW monocytic chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
XX Gudas JM, Haak-Frendescho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;

```

```

XX WPI; 2004-203794/19.
DR N-PSDB; ADK52349.
XX
PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 56; 154pp; English.
XX
CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX
SQ Sequence 152 AA;
XX
Query Match 93.1%; Score 523; DB 8; Length 152;
Best Local Similarity 92.5%; Pred. No. 2.2e-31;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
Db 1 DIQMTQSPSSLSASVGRVTITTCQASQDITVLNMYQKPGKAPKLLIYDASNLETVGPS 60
QY 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
Db 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDNLPLTFGGGTKEIK 107
XX
RESULT 13
ADD28243
ID ADD28243 standard; protein; 164 AA.
XX
AC ADD28243;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heterodimeric antibody light chain kappa region SEQ ID NO:21.
XX
KW human heterodimeric antibody; human; antibody; binding affinity;
KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003076568-A2.
XX
PD 18-SEP-2003.
XX
PF 11-FEB-2003; 2003WO-US004206.
XX
PR 11-FEB-2002; 2002US-0356086P.
PR 29-APR-2002; 2002US-0376408P.
PR 27-SEP-2002; 2002US-0414053P.
PR 25-NOV-2002; 2002US-0428807P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
XX Bowdish KS, Wild MA;
PI

```

XX WPI; 2003-722327/68.  
 XX  
 XX New human heterodimeric antibodies or their antibody fragments, useful as  
 PT anti-toxins or anti-infectives with respect to infective agents, e.g.  
 PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West  
 PT Nile virus.  
 XX  
 XX Claim 7; SEQ ID NO 21; 67pp; English.  
 XX  
 XX The present invention describes a human heterodimeric antibody (I)  
 CC (fragment) having a binding affinity of at least 1x10<sup>-8</sup> M to the  
 CC protective antigen of Bacillus anthracis or a molecule involved in  
 CC anthrax infection that blocks binding of the antigen or molecule to cell  
 CC receptors, edema factor and lethal factor. (I) has virucide and  
 CC antibacterial activities, and can be used in immunotherapy. The  
 CC antibodies (I) are useful as anti-toxins or anti-infectives with respect  
 CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan  
 CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The  
 CC kappa region sequence represents a human heterodimeric antibody light chain  
 CC present sequence represents a human heterodimeric antibody light chain  
 CC the present invention.  
 XX  
 XX Sequence 164 AA;

Query Match 93.1%; Score 523; DB 7; Length 164;  
 Best Local Similarity 93.5%; Pred. No. 2.4e-31;  
 Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNNYLNWYQKPGKAPKLLIYDASNLETVGPS 60  
 Db 3 DIQMTQSPSSLSASVGRVTITCOASQDINNNYLNWYQKPGKAPKLLIYDASNLETVGPS 62  
 QY 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDPLPLTFGGGTKEIK 107  
 Db 63 RFGSGSGTDFTTISGLQPEDIATYYCQYDNLGVTFGGTKEIK 109

RESULT 14  
 ADN97515  
 ID ADN97515 standard; protein; 502 AA.  
 XX  
 XX ADN97515;  
 XX  
 XX 01-JUL-2004 (first entry)  
 XX  
 XX Artificial protein construction protein #16.  
 XX  
 XX Artificial propeptide; propeptide; protein engineering; antibody.  
 XX  
 XX Unidentified.  
 XX  
 XX WO2004031362-A2.  
 XX  
 XX 15-APR-2004.  
 XX  
 XX 03-OCT-2003; 2003WO-US031420.  
 XX  
 XX 03-OCT-2002; 2002US-0415940P.  
 XX  
 XX (LARG-) LARGE SCALE BIOLOGY CORP.  
 XX  
 XX Reini SJ, Edwards P;  
 XX  
 XX WPI; 2004-330170/30.  
 XX  
 XX N-PSDB; ADN97514.  
 XX  
 XX New artificial propeptide comprises three peptide sequences, useful for  
 PT artificial multimeric protein engineering in eukaryotes.  
 XX  
 XX Example 2; SEQ ID NO 88; 244pp; English.  
 XX  
 XX The invention relates to an artificial propeptide comprising three

CC peptide sequences: a first peptide sequence of interest, a propeptide  
 CC sequence attached to the C-terminus of the first peptide sequence of  
 CC interest, and a second peptide of interest attached to the C-terminus of  
 CC the propeptide sequence. The artificial propeptide and polynucleotides  
 CC are useful for artificial multimeric protein engineering, e.g. antibodies  
 CC and antibody fragments in eukaryotes. This sequence corresponds to a  
 CC protein used in the generation of the protein of the invention.  
 XX  
 XX Sequence 502 AA;

Query Match 92.7%; Score 521; DB 8; Length 502;  
 Best Local Similarity 92.5%; Pred. No. 9.3e-31;  
 Matches 99; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNNYLNWYQKPGKAPKLLIYDASNLETVGPS 60  
 Db 23 DIQMTQSPSSLSASVGRVTITCOASQDINNNYLNWYQKPGKAPKLLIYDASNLETVGPS 82  
 QY 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDPLPLTFGGGTKEIK 107  
 Db 83 RFGSGSGTDFTTISGLQPEDIATYYCQYDNLPLTFGGGTKEIK 129

RESULT 15  
 ADD93785  
 ID ADD93785 standard; protein; 236 AA.  
 XX  
 XX ADD93785;  
 XX  
 XX 29-JAN-2004 (first entry)  
 XX  
 XX Monoclonal antibody 20.13.3 light chain.  
 DE  
 XX Monoclonal antibody; antibody; antiasthmatic; antiallergic;  
 KW antiinflammatory; immunosuppressive; dermatological;  
 KW gastrointestinal-gen.; antihelminthic; cytostatic; ophthalmological;  
 KW gastrodilator; interleukin-5; human; gene therapy.  
 XX  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..22 /note= "Signal peptide"  
 FT Protein 23..236 /note= "Light chain"  
 FT Misc-difference 23..130 /note= "Region specifically described in Claim 2"  
 FT Misc-difference 46..119 /note= "Region specifically described in Claim 2"  
 FT Region 46..56 /note= "CDR1"  
 FT Region 72..78 /note= "CDR2"  
 FT Region 111..119 /note= "CDR3"  
 XX  
 XX WO2003085089-A2.  
 XX  
 XX 16-OCT-2003.  
 XX  
 XX 27-MAR-2003; 2003WO-US009260.  
 XX  
 XX 29-MAR-2002; 2002US-0369044P.  
 XX  
 XX (SCHE ) SCHERING CORP.  
 XX (ABGE-) ABGENIX INC.  
 XX  
 XX Greenfeder S, Corvalan J;  
 XX  
 XX WPI; 2003-804302/75.  
 XX  
 XX N-PSDB; ADD93784.  
 XX  
 XX New antibody or its antigen-binding fragment that specifically binds



THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-26  
Perfect score: 562  
Sequence: 1 DIQMTQSPSSLSASVGDVRT.....CQQYDTLPLTFGGGTVKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	522	92.9	129	S52789	Ig kappa chain V r
2	517	92.0	108	K1HUAG	Ig kappa chain V-I
3	515	91.6	110	S44118	Ig kappa chain V-J
4	508	90.4	108	K1HURY	Ig kappa chain V-I
5	505	89.9	108	K1HUAU	Ig kappa chain V-I
6	496	88.3	139	S40365	Ig kappa chain - h
7	490	87.2	108	I39154	Ig kappa chain (BR
8	486	86.5	108	K1HURE	Ig kappa chain V-I
9	485	86.3	117	S42263	Ig kappa chain V r
10	485	86.3	117	S43528	Ig kappa chain V r
11	479	85.2	95	PH0862	Ig kappa chain V r
12	479	85.2	108	S49047	Ig kappa chain V r
13	476	84.7	125	S40349	Ig kappa chain V-J
14	475	84.5	108	K1HULY	Ig kappa chain V-I
15	473	84.2	107	S36264	Ig kappa chain V
16	473	84.2	108	K1HUSW	Ig kappa chain V-I
17	470	83.6	95	PH0864	Ig kappa chain V r
18	470	83.6	124	S40348	Ig kappa chain V-J
19	468	83.3	108	S19674	Ig kappa chain V r
20	465	82.7	123	S40331	Ig kappa chain - h
21	465	82.7	127	S40367	Ig kappa chain V-J
22	464	82.6	129	S52793	Ig kappa chain V r
23	462	82.2	135	S24320	Ig kappa chain pre
24	461	82.0	131	S40352	Ig kappa chain V-J
25	460	81.9	129	S40317	Ig kappa chain - h
26	459	81.7	108	S36279	Ig kappa chain V
27	459	81.7	125	S40333	Ig kappa chain V-J
28	458	81.5	107	S36269	Ig kappa chain V
29	458	81.5	125	S40316	Ig kappa chain - h

ALIGNMENTS

RESULT 1

S52789  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: S52789  
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995  
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-  
A:Reference number: S52789  
A:Accession: S52789  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <ROC>  
A:Cross-references: EMBL:X85995; NID:G758588; PIDN:CAA5987.1; PID:G758589  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 522; DB 2; Length 129;  
Best Local Similarity 92.5%; Pred. No. 3.6e-38;  
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDVRTITCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPS 60  
Db 23 DIQMTQSPSSLSASVGDVRTITCQASQDISNLYNQKPGKAPKLLIHAASSLETGVPS 82  
QY 61 RPSGSGSGTDFTTTISGLQPEDIATYYCOQYDTLPLTFGGGTVKVEIK 107  
Db 83 RPSGSGSGTDFTTTISGLQPEDLATYYCOQYDNLPLTFGGGTVKVEIK 129

RESULT 2

K1HUAG  
Ig kappa chain V-I region (Ag) - human  
C:Species: Homo sapiens (man)  
C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C:Accession: A01861  
R:Titani, K.; Shinoda, T.; Putnam, F.W.  
J. Biol. Chem. 244, 3550-3560, 1969  
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete  
A:Reference number: A92047; MUID:69234734; PMID:4893682  
A:Accession: A01861  
A:Molecule type: protein  
A:Residues: 1-108 <TIT>  
A:Cross-references: UNIPROT:P01593  
A>Note: the sequence of the C region, which has the Inv (3) marker, is also given  
C:Comment: This is a Bence Jones protein.  
C:Genetics:  
A:Gene: GDB:IGKV1  
A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12



QY 1 DIQMTQSPSSLSASVSGDRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETVGPS 60  
Db 1 DIQMTQSPSSLSASVSGDRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETVGPS 60  
QY 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDPLPLTFGGGTVKVEIK 107  
Db 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDPLPLTFGGGTVKVEIK 107

RESULT 6  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40365  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40365  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-139 <KLE>  
A:Cross-references: EMBL:X72475; NID:g441418; PIDN:CAA51143.1; PID:g441419  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 496; DB 2; Length 139;  
Best Local Similarity 88.8%; Pred. No. 6.7e-36;  
Matches 95; Conservative 1; Mismatches 11; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVSGDRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETVGPS 60  
Db 16 DIQMTQSPSSLSASVSGDRVTITCOATQDIGNLYNWYQKPGKAPKLLIYDASNLETVGPS 75  
QY 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDPLPLTFGGGTVKVEIK 107  
Db 76 RFGSGSGDTFTTISGLQPEDIATYCCQYDPLPLTFGGGTVKVEIK 122

RESULT 7  
Ig kappa chain (BRE) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 21-Jan-2000  
C:Accession: I39154  
R:Schormann, N.; Murrell, J.R.; Liepnies, J.J.; Benson, M.D.  
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995  
A:Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed  
A:Reference number: I39154; MUID:96003804; PMID:7568160  
A:Accession: I39154  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-108 <RES>  
A:Cross-references: EMBL:U31344; NID:g944925; PIDN:AAA79238.1; PID:g944926  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 490; DB 2; Length 108;  
Best Local Similarity 88.8%; Pred. No. 1.7e-35;  
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVSGDRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETVGPS 60  
Db 1 DIQMTQSPSSLSASVSGDRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASTLETGPS 60  
QY 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDPLPLTFGGGTVKVEIK 107  
Db 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDPLPLTFGGGTVKVEIK 107

RESULT 8  
Ig kappa chain V-I region (Rel) - human (tentative sequence)  
C:Species: Homo sapiens (man)  
C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C:Accession: A91663; A01873  
R:Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975  
A:Title: Die Primärstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom ka  
vollstaendige Aminosaeuresequenz des Proteins.  
A:Reference number: A91663; MUID:76023758; PMID:809329  
A:Accession: A91663  
A:Molecule type: Protein  
A:Residues: 1-108 <PAL>  
A:Cross-references: UNIPROT:P01607  
A>Note: the C region of this chain has the Inv (1,2) marker  
R:Epp, O.; Lattman, E.B.; Schiffer, M.; Huber, R.; Palm, W.  
Biochemistry 14, 4943-4952, 1975  
A:Title: The molecular structure of a dimer composed of the variable portions of the Ben  
A:Reference number: A90392; MUID:76039968; PMID:1182131  
A:Contents: annotation; X-ray crystallography, 2.0 angstroms  
C:Comment: This is a Bence Jones protein.  
C:Genetics:  
A:Gene: GDB:IGKV1  
A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapi  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status experimental

Query Match 86.5%; Score 486; DB 1; Length 108;  
Best Local Similarity 86.8%; Pred. No. 3.8e-35;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVSGDRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETVGPS 60  
Db 1 DIQMTQSPSSLSASVSGDRVTITCOASQDIKLYLNWYQKPGKAPKLLIYEASNLQGVPS 60  
QY 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDPLPLTFGGGTVKVEI 106  
Db 61 RFGSGSGDTFTTISGLQPEDIATYCCQYDPLPLTFGGGTVKVEI 106

RESULT 9  
Ig kappa chain V region (08) - human  
C:Species: Homo sapiens (man)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S42263  
R:Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Quer  
J. Immunol. 147, 4007-4013, 1991  
A:Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf  
A:Reference number: S42263; MUID:92043792; PMID:1940382  
A:Accession: S42263  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-117 <SCO>  
A:Cross-references: EMBL:M64855; NID:g185963; PIDN:AAA58925.1; PID:g185964  
C:Genetics:  
A:Insertions: 19/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 485; DB 2; Length 117;  
Best Local Similarity 96.8%; Pred. No. 5e-35;  
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVSGDRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETVGPS 60

```
Db      23 DIQWTQSPSSLSASVGDRTVITTCASQDINSYLNWYQKPGKAPKLLIYDASNLETGVPS 82
Qy      61 RFSGSGGTDTFTTISGLQPEDIATYYCQYDTLP 95
Db      83 RFSGSGGTDTFTTISGLQPEDIATYYCQYDNLP 117

RESULT 10
S43528
Ig kappa chain V region (018) - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: S43528
R;Scott, M.G.; Crimmings, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
submitted to the EMBL Data Library, December 1991
A;Reference number: S43528
A;Accession: S43528
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <SCO>
A;Cross-references: EMBL:M64856
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match      86.3%; Score 485; DB 2; Length 117;
Best Local Similarity 96.8%; Pred. No. 5e-35;
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DIQWTQSPSSLSASVGDRTVITTCASQDINSYLNWYQKPGKAPKLLIYDASNLETGVPS 60
Db      23 DIQWTQSPSSLSASVGDRTVITTCASQDINSYLNWYQKPGKAPKLLIYDASNLETGVPS 82

Qy      61 RFSGSGGTDTFTTISGLQPEDIATYYCQYDTLP 95
Db      83 RFSGSGGTDTFTTISGLQPEDIATYYCQYDNLP 117

RESULT 11
PH0862
Ig kappa chain V region (anti-DNA, Iii-3R) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0862
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0862
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

Query Match      85.2%; Score 479; DB 2; Length 95;
Best Local Similarity 95.8%; Pred. No. 1.3e-34;
Matches 91; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DIQWTQSPSSLSASVGDRTVITTCASQDINSYLNWYQKPGKAPKLLIYDASNLETGVPS 60
Db      1 DIQWTQSPSSLSASVGDRTVITTCASQDINSYLNWYQKPGKAPKLLIYDASNLETGVPS 60

Qy      61 RFSGSGGTDTFTTISGLQPEDIATYYCQYDTLP 95
```

```
Db      61 RISGSGGTDTFTTISGLQPEDIATYYCQYDNLP 95

RESULT 12
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match      85.2%; Score 479; DB 2; Length 108;
Best Local Similarity 86.0%; Pred. No. 1.5e-34;
Matches 92; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy      1 DIQWTQSPSSLSASVGDRTVITTCASQDINSYLNWYQKPGKAPKLLIYDASNLETGVPS 60
Db      1 DIQWTQSPSSLSASVGDRTVITTCASQDINSYLNWYQKPGKAPKLLIYDASNLETGVPS 60

Qy      61 RFSGSGGTDTFTTISGLQPEDIATYYCQYDTLP 107
Db      61 RFSGSGGTDTFTTISGLQPEDIATYYCQYDTLP 107

RESULT 13
S40349
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S40349
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40349
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match      84.7%; Score 476; DB 2; Length 125;
Best Local Similarity 85.8%; Pred. No. 3.2e-34;
Matches 91; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy      2 IQMTQSPSSLSASVGDRTVITTCASQDINSYLNWYQKPGKAPKLLIYDASNLETGVPSR 61
Db      19 IQLTQSPSSLSASVGDRTVITTCASQGISALAWYQKPGKAPKLLIYDASSLESQVPSR 78

Qy      62 FSGSGGTDTFTTISGLQPEDIATYYCQYDTLP 107
Db      79 FSGSGGTDTFTTISGLQPEDIATYYCQYDTLP 124

RESULT 14
KHULY
Ig kappa chain V-I region (Iay) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
```



Search completed: November 16, 2005, 22:04:09  
Job time : 13.7849 secs

**Qy**

61 RFSGSGTDFTTISGLQPEDIAYYCQYDTIPLTFGGGKVEIK 107  
||||| ||| ||| ||| ||| ||| ||| ||| ||| :||  
**Db**

61 RFSGSGTDFLTISLQPEFATYYCOYSNPFLTFFGGTKVDIK 107

THIS PAGE BLANK (UCPTC)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-26  
Perfect score: 562  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQQYDTLPLTGGGKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	92.0	108	1 KV1A_HUMAN	P01593 homo sapien
2	510	90.7	108	1 KV1Y_HUMAN	P80362 homo sapien
3	508	90.4	108	1 KV1P_HUMAN	P01608 homo sapien
4	505	89.9	108	1 KV1B_HUMAN	P01594 homo sapien
5	486	86.5	108	1 KV1O_HUMAN	P01607 homo sapien
6	475	84.5	108	1 KV1M_HUMAN	P01605 homo sapien
7	473	84.2	108	1 KV1Q_HUMAN	P01609 homo sapien
8	468	83.3	236	2 Q6GMX0	Q6gmxx0 homo sapien
9	467.5	83.2	107	2 Q96SA9	Q96sa9 homo sapien
10	459	81.7	108	2 Q9UL70	Q9ul70 homo sapien
11	456	81.1	108	1 KV1K_HUMAN	P01603 homo sapien
12	453	80.6	108	1 KV1C_HUMAN	P01595 homo sapien
13	453	80.6	236	2 Q723Y4	Q723y4 homo sapien
14	452	80.4	108	1 KV1S_HUMAN	P01611 homo sapien
15	452	80.4	108	2 Q9UL77	Q9ul77 homo sapien
16	452	80.4	236	2 Q6GMX9	Q6gmxx9 homo sapien
17	451	80.2	129	1 KV1W_HUMAN	P04431 homo sapien
18	450	80.1	236	2 Q6GMX8	Q6gmxx8 homo sapien
19	450	80.1	244	2 Q65ZC8	Q65zc8 homo sapien
20	448	79.7	108	1 KV1E_HUMAN	P01597 homo sapien
21	448	79.7	112	1 KV1U_HUMAN	P01613 homo sapien
22	448	79.7	236	2 Q6PIH7	Q6pih7 homo sapien
23	446.5	79.4	107	2 Q9UL81	Q9ul81 homo sapien
24	446	79.4	108	1 KV1V_HUMAN	P04430 homo sapien
25	445	79.2	116	2 Q96PF6	Q96pf6 homo sapien
26	445	79.2	240	2 Q65ZC9	Q65zc9 homo sapien
27	442	78.6	108	1 KV1H_HUMAN	P01600 homo sapien
28	438	77.9	236	2 Q6GMW1	Q6gmw1 homo sapien
29	436	77.6	108	1 KV1F_HUMAN	P01598 homo sapien
30	436	77.6	108	1 KV1R_HUMAN	P01610 homo sapien
31	435	77.4	236	2 Q6PIH4	Q6pih4 homo sapien

ALIGNMENTS

RESULT 1

ID	KV1A_HUMAN	STANDARD;	PRT;	108 AA.
AC	P01593;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ig kappa chain V-I region AG.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=69234734; PubMed=4893682;			
RA	Titani K., Shinoda T., Putnam F.W.;			
RT	"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";			
RL	J. Biol. Chem. 244:3550-3560(1969).			
CC	-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.			
CC	-!- MISCELLANEOUS: This is a Bence-Jones protein.			
DR	PIR; A01861; K1HUAG.			
DR	HSSP; P01607; 1BWV.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Bence-Jones protein; Direct protein sequencing;			
FT	DOMAIN 1 23			
FT	DOMAIN 24 34			
FT	DOMAIN 35 49			
FT	DOMAIN 50 56			
FT	DOMAIN 57 88			
FT	DOMAIN 89 97			
FT	DOMAIN 98 107			
FT	DISULFID 23 88			
FT	NON TER 108 108			
SQ	SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;			

Query Match 92.0%; Score 517; DB 1; Length 108;  
Best Local Similarity 92.5%; Pred. No. 2.6e-43;  
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy	1	DIQMTQSPSSLSASVGRVTITTCQASQDINNYLNWYQQKPKAPKLLIYDASNLTGVPS	60
Db	1	DIQMTQSPSSLSASVGRVTITTCQASQDINHYLNWYQQKPKAPKLLIYDASNLTGVPS	60
Qy	61	RFGSGSGSTDTFTTISGLQPSDIIATYYCQYDTLPLTFTGGGKVEIK	107

Db	61	RFSGSGGTDFTFTISGLQPEDIAIYYCQYDTLPRTFGGTKLEIK	107
RESULT 2			
ID	KV1Y_HUMAN	STANDARD; PRT; 108 AA.	
AC	P80362;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Ig kappa chain V-I region VAR.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).		
RX	MEDLINE=95086080; PubMed=7993911;		
RA	Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,		
RA	Solomon A., Stevens F.J., Schiffer M.;		
RT	"Comparison of crystal structures of two homologous proteins:		
RT	Structural origin of altered domain interactions in immunoglobulin		
RT	light-chain dimers.";		
RL	Biochemistry 33:14848-14857(1994).		
RN	[2]		
RP	SEQUENCE OF 1-35.		
RX	MEDLINE=81367384; PubMed=6167731;		
RA	Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,		
RA	Popp R.A., Solomon A.;		
RT	"Characterization and preliminary crystallographic data on the VL-		
RT	related fragment of the human ki Bence Jones protein wat.";		
RL	J. Mol. Biol. 147:185-193(1981).		
CC	-!- MISCELLANEOUS: This is a Bence-Jones protein.		
DR	PDB; 1WIL; X-ray; A/B=1-108.		
DR	GO; GO:0005576; C:extracellular; NAS.		
DR	GO; GO:0003823; F:antigen binding; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG LIKE; 1.		
DR	3D-structure; Bence-Jones protein; Direct protein sequencing;		
KW	Immunoglobulin V region.		
FT	DOMAIN 1 23	Framework-1.	
FT	DOMAIN 24 34	Complementarity-determining-1.	
FT	DOMAIN 35 49	Framework-2.	
FT	DOMAIN 50 56	Complementarity-determining-2.	
FT	DOMAIN 57 88	Framework-3.	
FT	DOMAIN 89 97	Complementarity-determining-3.	
FT	DOMAIN 98 107	Framework-4.	
FT	DISULFID 23 88	By similarity.	
FT	CONFLICT 30 31	TN -> SD (in Ref. 2).	
FT	STRAND 4 7		
FT	STRAND 10 13		
FT	TURN 15 16		
FT	TURN 19 25		
FT	TURN 30 31		
FT	STRAND 33 38		
FT	TURN 40 41		
FT	STRAND 45 49		
FT	TURN 50 52		
FT	STRAND 53 54		
FT	TURN 56 57		
FT	TURN 60 61		
FT	STRAND 62 67		
FT	TURN 68 69		
FT	TURN 70 75		
FT	HELIX 80 82		
FT	STRAND 84 90		
FT	STRAND 98 98		
FT	STRAND 102 106		
FT	NON_TER 108 108		
SQ			
SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAB697 CRC64;			
Query Match 90.7%; Score 510; DB 1; Length 108;			
Best Local Similarity 89.7%; Pred. No. 1.3e-42;			
Matches 96; Conservative 7; Mismatches 4; Indels 0; Gaps 0;			
RESULT 3			
ID	KV1P_HUMAN	STANDARD; PRT; 108 AA.	
AC	P01608;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Ig kappa chain V-I region Roy.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=68362076; PubMed=5595110;		
RA	Hiltschmann N.;		
RT	"Chemical structure of 2 kappa-type Bence Jones proteins (Roy and		
RT	Cum.).";		
RL	Hoppe-Seyley's Z. Physiol. Chem. 348:1077-1080(1967).		
RN	[2]		
RP	REVISIONS TO 39 AND 41.		
RA	Hiltschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,		
RA	Steinmetz-Kayne M., Suter L., Watanabe S.;		
RL	(In) Franek F., Shugar D. (eds.);		
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New		
RL	York (1969).		
CC	-!- MISCELLANEOUS: The C region of this chain has the INV (1,2)		
CC	marker.		
CC	-!- MISCELLANEOUS: This is a Bence-Jones protein.		
DR	PIR; A91638; KIHURY.		
DR	HSP; P01607; LBWW.		
DR	GO; GO:0005576; C:extracellular; NAS.		
DR	GO; GO:0003823; F:antigen binding; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG LIKE; 1.		
DR	Bence-Jones protein; Direct protein sequencing;		
KW	Immunoglobulin V region.		
FT	DOMAIN 1 23	Framework-1.	
FT	DOMAIN 24 34	Complementarity-determining-1.	
FT	DOMAIN 35 49	Framework-2.	
FT	DOMAIN 50 56	Complementarity-determining-2.	
FT	DOMAIN 57 88	Framework-3.	
FT	DOMAIN 89 97	Complementarity-determining-3.	
FT	DOMAIN 98 107	Framework-4.	
FT	DISULFID 23 88	By similarity.	
FT	NON_TER 108 108		
SQ	SEQUENCE 108 AA; 11782 MW; FSACEDE5A313DF3A CRC64;		
Query Match 90.4%; Score 508; DB 1; Length 108;			
Best Local Similarity 89.7%; Pred. No. 2e-42;			
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;			
SQ			
SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAB697 CRC64;			
Query Match 90.7%; Score 510; DB 1; Length 108;			
Best Local Similarity 89.7%; Pred. No. 1.3e-42;			
Matches 96; Conservative 7; Mismatches 4; Indels 0; Gaps 0;			
RESULT 4			
ID	KV1Y_HUMAN	STANDARD; PRT; 108 AA.	
AC	P80362;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Ig kappa chain V-I region VAR.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).		
RX	MEDLINE=95086080; PubMed=7993911;		
RA	Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,		
RA	Solomon A., Stevens F.J., Schiffer M.;		
RT	"Comparison of crystal structures of two homologous proteins:		
RT	Structural origin of altered domain interactions in immunoglobulin		
RT	light-chain dimers.";		
RL	Biochemistry 33:14848-14857(1994).		
RN	[2]		
RP	SEQUENCE OF 1-35.		
RX	MEDLINE=81367384; PubMed=6167731;		
RA	Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,		
RA	Popp R.A., Solomon A.;		
RT	"Characterization and preliminary crystallographic data on the VL-		
RT	related fragment of the human ki Bence Jones protein wat.";		
RL	J. Mol. Biol. 147:185-193(1981).		
CC	-!- MISCELLANEOUS: This is a Bence-Jones protein.		
DR	PDB; 1WIL; X-ray; A/B=1-108.		
DR	GO; GO:0005576; C:extracellular; NAS.		
DR	GO; GO:0003823; F:antigen binding; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG LIKE; 1.		
DR	3D-structure; Bence-Jones protein; Direct protein sequencing;		
KW	Immunoglobulin V region.		
FT	DOMAIN 1 23	Framework-1.	
FT	DOMAIN 24 34	Complementarity-determining-1.	
FT	DOMAIN 35 49	Framework-2.	
FT	DOMAIN 50 56	Complementarity-determining-2.	
FT	DOMAIN 57 88	Framework-3.	
FT	DOMAIN 89 97	Complementarity-determining-3.	
FT	DOMAIN 98 107	Framework-4.	
FT	DISULFID 23 88	By similarity.	
FT	CONFLICT 30 31	TN -> SD (in Ref. 2).	
FT	STRAND 4 7		
FT	STRAND 10 13		
FT	TURN 15 16		
FT	TURN 19 25		
FT	TURN 30 31		
FT	STRAND 33 38		
FT	TURN 40 41		
FT	STRAND 45 49		
FT	TURN 50 52		
FT	STRAND 53 54		
FT	TURN 56 57		
FT	TURN 60 61		
FT	STRAND 62 67		
FT	TURN 68 69		
FT	TURN 70 75		
FT	HELIX 80 82		
FT	STRAND 84 90		
FT	STRAND 98 98		
FT	STRAND 102 106		
FT	NON_TER 108 108		

Db 1 DIQMTQSPSSLSASVGRVTITCSQSDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60  
QY 61 RFGSGSGDTFTTISGLQPEDIAIYCCQYDPLPLTFGGGKVEIK 107  
Db 61 RFGSGSGDTFTTISGLQPEDIAIYCCQYDPLPLTFGGGKVEIK 107  
RESULT 4  
KV10 HUMAN STANDARD; PRT; 108 AA.  
AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig kappa chain V-I region AU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72189444; PubMed=5028201;  
RA Schiechl H., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
protein Au).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).  
RN [2]  
RX RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehnammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
Schwager P., Steigemann W., Schramm H.J.;  
RT "The structure determination of the variable portion of the Bence-  
Jones protein Au.";  
RL Biophys. Struct. Mech. 1:139-146 (1975).  
CC -!- MISCELLANEOUS: The structure of the V region was determined by  
molecular replacement methods using the known structure of the V  
region of the kappa chain REI.  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; A91653; KIHUAE.  
DR PDB; 1JW5; X-ray; A/B=1-107.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.  
FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT STRAND 4 5  
FT STRAND 10 13  
FT TURN 15 16  
FT TURN 19 25  
FT TURN 30 31  
FT STRAND 33 38  
FT TURN 40 41  
FT STRAND 44 49  
FT TURN 50 52  
FT STRAND 53 54  
FT TURN 56 57  
FT TURN 60 61  
FT STRAND 62 67

FT TURN 68 69  
FT STRAND 70 75  
FT HELIX 80 82  
FT STRAND 85 90  
FT STRAND 97 98  
FT STRAND 102 106  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6F6FB9 CRC64;  
Query Match 89.9%; Score 505; DB 1; Length 108;  
Best Local Similarity 90.7%; Pred. No. 4e-42;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTITCSQSDINNNVYQQKPGKAPKLLIYDASNLETGVP 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSQSDISIFLNWYQQKPGKAPKLLIYDASNLETGVP 60  
QY 61 RFGSGSGDTFTTISGLQPEDIAIYCCQYDPLPLTFGGGKVEIK 107  
Db 61 RFGSGSGDTFTTISGLQPEDIAIYCCQYDPLPLTFGGGKVEIK 107  
RESULT 5  
KV10 HUMAN STANDARD; PRT; 108 AA.  
AC P01607;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig kappa chain V-I region REI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76023758; PubMed=809329;  
RA Palm W., Hilschmann N.;  
RT "The primary structure of a crystalline monoclonal immunoglobulin  
kappa-type L-chain, subgroup I (Bence-Jones protein REI); isolation  
and characterization of the tryptic peptides; the complete amino acid  
sequence of the protein; a contribution to the elucidation of the  
three-dimensional structure of antibodies, in particular their  
combining site.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).  
RN [2]  
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=76039968; PubMed=1182131;  
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;  
RT "The molecular structure of a dimer composed of the variable portions  
of the Bence-Jones protein REI refined at 2.0-A resolution.";  
Biochemistry 14:4943-4952 (1975).  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
marker.  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
CC PIR; A91663; KIHURE.  
DR PDB; 1AR2; X-ray; @=1-107.  
DR PDB; 1BWW; X-ray; A/B=1-107.  
DR PDB; 1REI; X-ray; A/B=1-107.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88  
FT STRAND 4 7  
FT STRAND 10 13  
FT TURN 15 16  
FT STRAND 19 25  
FT TURN 30 31  
FT STRAND 33 38  
FT TURN 40 41  
FT STRAND 45 49  
FT TURN 50 52  
FT STRAND 53 54  
FT TURN 56 57  
FT TURN 60 61  
FT STRAND 62 67  
FT TURN 68 69  
FT STRAND 70 75  
FT HELIX 80 82  
FT STRAND 84 90  
FT STRAND 97 98  
FT STRAND 102 106  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 9E8143E1188BCE2A CRC64;

Query Match 86.5%; Score 486; DB 1; Length 108;  
Best Local Similarity 86.8%; Pred. No. 3e-40;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCAQSDINNYLNWYQKPGKAPKLLIYDASNLTGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCAQSDIITKYNWYQKPGKAPKLLIYASNLQGVPS 60

QY 61 RFGSGSGTDFTFTISGLQPEDIATYYCQYDTLPLTFGGGTKEI 106  
DB 61 RFGSGSGTDYFTFTISGLQPEDIATYYCQYQSLPYTFGGGTKEI 106

RESULT 6  
KV1M HUMAN STANDARD; PRT; 108 AA.  
AC P01605;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-1 region Lay.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77038198; PubMed=824717;  
RA Capra J.D., Klapper D.G.;  
RT "Complete amino acid sequence of the variable domains of two human IgM  
anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";  
RL Scand. J. Immunol. 5:677-684(1976).  
CC -!- MISCELLANEOUS: The second and third hypervariable regions of this  
chain are identical with those of the human POM V-III kappa chain,  
with which it shares certain idiotypic determinants.  
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma  
globulin activity.  
CC PIR; A01871; KIHULY.  
DR HSSP; P01607; 1BWW.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR Pfam; PF00047; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.

KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.  
FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 84.5%; Score 475; DB 1; Length 108;  
Best Local Similarity 85.0%; Pred. No. 3.7e-39;  
Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCAQSDINNYLNWYQKPGKAPKLLIYDASNLTGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCAQSONVAYLNWYQKPGKAPKLLIYGASTREAGVPS 60

QY 61 RFGSGSGTDFTFTISGLQPEDIATYYCQYDTLPLTFGGGTKEIK 107  
DB 61 RFGSGSGTDFTFTISGLQPEDIATYYCQYNNWPPPTFGGTKEVVK 107

RESULT 7  
KV1Q HUMAN STANDARD; PRT; 108 AA.  
AC P01609;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-1 region Scw.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75059271; PubMed=4435756;  
RA Eulitz M., Hilschmann N.;  
RT "The primary structure of a human immunoglobulin L-chain of kappa-type  
(Bence-Jones protein Scw.), II: the chymotryptic peptides and the  
complete amino acid sequence.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
marker.  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
CC PIR; A01875; KIHUSW.  
DR HSSP; P01607; 1BWW.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.

KW Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.  
FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11764 MW; 32CEDDDF9644414 CRC64;

Query Match 84.2%; Score 473; DB 1; Length 108;  
Best Local Similarity 84.1%; Pred. No. 5.8e-39;

```
Matches 90; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITTCQASQDINRKLHWYDQKPGKAPRLIYDASNLETGVPS 60
QY 61 RESGSGSGTDFTTISGLQPEDIAIYCCQYDTLPLTFGGGKVEIK 107
DB 61 RESGSGSGTDFTTISGLQPEDIGNYYCCQYDNNVPIITFGGTRVENK 107

RESULT 8
Q6GMX0 PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 83.3%; Score 468; DB 2; Length 236;
Best Local Similarity 83.2%; Pred. No. 4.3e-38;
Matches 99; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
```

```
Matches 93; Conservative 6; Mismatches 6; Indels 3; Gaps 2;
QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITTCRASQSISSYLNLYQKPGKAPKLLIYDASNLETGVPS 60
QY 61 RESGSGSGTDFTTISGLQPEDIAIYCCQYDTLPLTFGGGKVEIK 107
DB 61 RESGSGSGTDFTTISGLQPEDFATYYCCQSYST--LTFGGGKVEIK 106

RESULT 9
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34085; S34086.
DR HSSP; P01607; 1BWV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match 83.2%; Score 467.5; DB 2; Length 107;
Best Local Similarity 86.1%; Pred. No. 2e-38;
Matches 93; Conservative 6; Mismatches 6; Indels 3; Gaps 2;
QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDINNVLNMYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITTCRASQSISSYLNLYQKPGKAPKLLIYDASNLETGVPS 60
QY 61 RESGSGSGTDFTTISGLQPEDIAIYCCQYDTLPLTFGGGKVEIK 107
DB 61 RESGSGSGTDFTTISGLQPEDFATYYCCQSYST--LTFGGGKVEIK 106

RESULT 10
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

```

RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 81.7%; Score 459; DB 2; Length 108;
Best Local Similarity 81.3%; Pred. No. 1.4e-37;
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVGRVTITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSLSASVGRVTITTCRASQGISNYLAWYQKPGKPKSLIYAASLTQSGVPS 60
QY 61 RFSGSGSGTDFTTISGLQPEDVATYYCQYQDTLPLTFGGGTKEIK 107
DB 61 RFSGSGSGTDFTTISGLQPEDVATYYCQKINSAPRTFGGTKEIK 107

RESULT 11
KV1K HUMAN STANDARD; PRT; 108 AA.
ID KV1K HUMAN
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA Shinoda T.;
RT "Comparative structural studies on the light chains of human
RT immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL J. Biochem. 77:1277-1296(1975).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01869; KIHUKA.
DR HSP; P80362; LWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Complementarity-determining-3.
FT DOMAIN 89 97 Complementarity-determining-4.
FT DOMAIN 98 107 By similarity.
FT DISULFID 23 88
FT NON_TER 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match 80.6%; Score 453; DB 1; Length 108;
Best Local Similarity 82.2%; Pred. No. 5.5e-37;
Matches 88; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVGRVTITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSLSASVGRVTITTCQASQDINSLIWTQQKPGKAPKFLIYDAENLETGVPS 60
QY 61 RFSGSGSGTDFTTISGLQPEDVATYYCQYQDTLPLTFGGGTKEIK 107
DB 61 RFRSGSGTDFALSISSLQPEDFATYYCQYQYNNLPYTFGGGTKEIK 107

Query Match 81.1%; Score 456; DB 1; Length 108;
Best Local Similarity 77.6%; Pred. No. 2.8e-37;
Matches 83; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVGRVTITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSLSASVGRVTITTCASQTVLSVLYNWYQKPGKAPKLLIYDASNLETGVPS 60
QY 61 RFSGSGSGTDFTTISGLQPEDVATYYCQYQDTLPLTFGGGTKEIK 107
DB 61 RFSGSGSGTDFTTISVZPZBFATYYCQYQYLDLPRTFGGTKEIK 107

RESULT 12
KV1C HUMAN STANDARD; PRT; 108 AA.
ID KV1C HUMAN
AC P01595;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Bi.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=73029807; PubMed=4563064;
RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT "Principle of antibody structure. The primary structure of a
RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
RT Bi). 3. The complete amino acid sequence and the genetic significance
RT of the variability principles for the mechanism of antibody
RT formation.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01863; KIHUBI.
DR HSP; P01607; IBMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Complementarity-determining-3.
FT DOMAIN 89 97 Complementarity-determining-4.
FT DOMAIN 98 107 By similarity.
FT DISULFID 23 88
FT NON_TER 108
SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

Query Match 80.6%; Score 453; DB 1; Length 108;
Best Local Similarity 82.2%; Pred. No. 5.5e-37;
Matches 88; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVGRVTITTCQASQDINNLYNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSLSASVGRVTITTCQASQDINSLIWTQQKPGKAPKFLIYDAENLETGVPS 60
QY 61 RFSGSGSGTDFTTISGLQPEDVATYYCQYQDTLPLTFGGGTKEIK 107
DB 61 RFRSGSGTDFALSISSLQPEDFATYYCQYQYNNLPYTFGGGTKEIK 107
```



```

RESULT 13
Q723Y4
AC Q723Y4 PRELIMINARY; PRT; 236 AA.
ID Q723Y4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal Muscle;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;

Query Match 80.6%; Score 453; DB 2; Length 236;
Best Local Similarity 80.4%; Pred. No. 1.3e-36;
Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETVGVS 60
DB 23 DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWFQKPGKAPKLLIYGASSLQSGVQS 82
QY 61 RPSGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
DB 83 RPSGSGSGTDTFTTISGLQPEDIATYCCQYKSPYPTFGGTKLEIK 129

RESULT 14
KV1S_HUMAN
ID KV1S_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)

Query Match 80.4%; Score 452; DB 1; Length 108;
Best Local Similarity 80.4%; Pred. No. 6.9e-37;
Matches 86; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCOASQDINNYLNWYQKPGKAPKLLIYDASNLETVGVS 60
DB 1 DIQMTQSPSSLSASVGDRVTITCRASQDISHLAWYQKSGKAPKLLIYSASSLENGVPS 60
QY 61 RPSGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
DB 61 RPSGSGSGTDTFTTISGLQPEDIATYCCQAHSVPLTFGGTVDIK 107

RESULT 15
Q9UL77
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357A-26  
Perfect score: 562  
Sequence: 1 DQMTQSPSSLSASVGRVT.....CQYDTLPLTFFGGTKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	93.4	107	1	US-08-276-852-108
2	525	93.4	107	1	US-08-899-575-108
3	525	93.4	107	1	US-08-899-575-108
4	525	93.4	107	5	PCT-US95-08743-108
5	503	89.5	107	2	US-08-318-157B-6
6	503	89.5	107	4	US-09-253-794-6
7	502	89.3	107	1	US-08-276-852-107
8	502	89.3	107	1	US-08-899-575-107
9	502	89.3	107	1	US-08-899-575-107
10	502	89.3	107	5	PCT-US95-08743-107
11	493	87.7	108	3	US-09-025-769B-14
12	493	87.7	108	4	US-09-490-070A-14
13	493	87.7	108	4	US-09-490-153-14
14	493	87.7	108	4	US-09-490-324-14
15	488	86.8	109	3	US-09-157-370-3
16	486	86.5	107	2	US-08-561-521-6
17	486	86.5	107	2	US-08-652-558-34
18	486	86.5	107	3	US-09-025-203-15
19	486	86.5	107	4	US-09-999-021-15
20	486	86.5	107	4	US-09-999-025-15
21	486	86.5	107	4	US-10-040-997-15
22	486	86.5	107	4	US-09-999-040-15
23	486	86.5	107	4	US-09-998-817-15
24	486	86.5	107	5	PCT-US95-01219-6
25	486	86.5	108	2	US-08-070-116A-7
26	486	86.5	108	2	US-08-116-247-9
27	486	86.5	108	4	US-08-557-050-7

28 486 86.5 108 4 US-08-454-899G-100 Sequence 100, Appl  
29 486 86.5 108 4 US-09-348-224-9 Sequence 9, Appl  
30 486 86.5 111 1 US-08-137-117D-67 Sequence 67, Appl  
31 486 86.5 111 2 US-08-436-717-67 Sequence 67, Appl  
32 486 86.5 126 1 US-08-137-117D-71 Sequence 71, Appl  
33 486 86.5 126 2 US-08-436-717-71 Sequence 71, Appl  
34 486 86.5 214 2 US-07-934-373C-39 Sequence 39, Appl  
35 486 86.5 214 3 US-08-437-642B-39 Sequence 39, Appl  
36 486 86.5 214 5 PCT-US93-07832-39 Sequence 39, Appl  
37 484 86.1 109 2 US-07-934-373C-3 Sequence 3, Appl  
38 484 86.1 109 3 US-08-437-642B-3 Sequence 3, Appl  
39 484 86.1 109 4 US-08-146-206C-3 Sequence 3, Appl  
40 484 86.1 109 4 US-09-705-686-3 Sequence 3, Appl  
41 484 86.1 109 4 US-09-705-392A-3 Sequence 3, Appl  
42 484 86.1 109 4 US-09-705-398-3 Sequence 3, Appl  
43 484 86.1 109 5 PCT-US93-07832-3 Sequence 3, Appl  
44 483 85.9 107 2 US-07-934-373C-18 Sequence 18, Appl  
45 483 85.9 107 3 US-08-437-642B-18 Sequence 18, Appl

## ALIGNMENTS

RESULT 1  
US-08-276-852-108  
; Sequence 108, Application US/08276852  
; Patent No. 5652138  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/276,852  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRI452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 108:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-276-852-108



```

GENERAL INFORMATION:
;
; APPLICATION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
;
; NUMBER OF SEQUENCES: 170
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: PCT/US95/08743
;
; FILING DATE: 11-JUL-1995
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 08/276,852
;
; FILING DATE: 18-JUL-1994
;
; INFORMATION FOR SEQ ID NO: 108:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 107 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; PCT-US95-08743-108

```

Query Match	93.4%	Score 525;	DB 5;	Length 107;
Best Local Similarity	94.3%;	Pred. No. 2.9e-42;		
Matches	99;	Conservative 4;	Mismatches 2;	Indels 0; Gaps 0;
Qy	3	QMTQSPSSLSASVGDRVTITCOASQDINNNYVQKPGKAPKLLIYDASNLETGVS	SRF 62	
Db	1	ELTQSPSSLSASVGDRVTITCOASQDISNHLNNYVQKPGKAPKLLIYDASNLETGVS	SRF 60	
		:	:	
Qy	63	SGSGSGTDFFTISGLQPEDIATYVCOQYDTLPLTFGGGKVK	107	
Db	61	SGSGSGTDFFTISLQPEDIATYVCOQYDNLTPLTFGGGKVK	105	

RESULT 5  
 US-08-318-157B-6  
 ; Sequence 6, Application US/08318157B  
 ; Patent No. 5874540  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HANSEN, Hans J.  
 ; APPLICANT: ARMOUR, Kathryn L.  
 ; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED  
 ; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES  
 ; NUMBER OF SEQUENCES: 58  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/318,157B  
 ; FILING DATE: 05-OCT-1994  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: SAXE, Bernhard D.  
 ; REGISTRATION NUMBER: 28,665  
 ; REFERENCE/DOCKET NUMBER: 18733/464  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-157B-6

Query Match      89.5%; Score 503; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.4e-40;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLASVGDVRVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLASVGDVRVITTCQASQDIITKLYNQKPGKAPKLLIYEASNLQAGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 RFSGSGSGTDFTTISLQLPEDIATYYCQOYDTLPLTFGGGTKEIK 107
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGTDFTTISLQLPEDIATYYCQOYSLPYTFGGGTKEIK 107
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-09-253-794-6
; Sequence 6, Application US/09253794
; Patent No. 6676924
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-253-794-6

Query Match      89.5%; Score 503; DB 4; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.4e-40;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLASVGDVRVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```





Db 1 DIQWTQSPSSLSASVGRVITTCRASQISNLYNWYQKPGKAPKLLIYAASSLQSGVPS 60  
Qy 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDYLPLTFGGGTKEIK 107  
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQYYSSTPLTFGGGTKEIK 107

RESULT 12

US-09-490-070A-14  
; Sequence 14, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & McAuliffe  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490.070A  
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2020  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-490-070A-14

Query Match 87.7%; Score 493; DB 4; Length 108;  
Best Local Similarity 87.9%; Pred. No. 3e-39;  
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQISNLYNWYQKPGKAPKLLIYAASSLQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGRVITTCRASQISNLYNWYQKPGKAPKLLIYAASSLQSGVPS 60  
Qy 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDYLPLTFGGGTKEIK 107  
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQYYSSTPLTFGGGTKEIK 107

RESULT 13

US-09-490-153-14  
; Sequence 14, Application US/09490153

; Patent No. 6706484  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490.153  
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025.769B  
FILING DATE: 18-FEB-1998

ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-490-153-14

Query Match 87.7%; Score 493; DB 4; Length 108;  
Best Local Similarity 87.9%; Pred. No. 3e-39;  
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGRVITTCRASQISNLYNWYQKPGKAPKLLIYAASSLQSGVPS 60  
Db 1 DIQWTQSPSSLSASVGRVITTCRASQISNLYNWYQKPGKAPKLLIYAASSLQSGVPS 60  
Qy 61 RFGSGSGTDFTTISGLQPEDIATYYCQYDYLPLTFGGGTKEIK 107  
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQYYSSTPLTFGGGTKEIK 107

RESULT 14

US-09-490-324-14  
; Sequence 14, Application US/09490324  
; Patent No. 6828422

GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373



;;  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
;; STREET: 1251 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10021  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA: US/09/490,324  
;; APPLICATION NUMBER: US/09/490,324  
;; FILING DATE: 24-Jan-2000  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/025,769  
;; FILING DATE: 18-FEB-1998  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 108 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-490-324-14

Query Match 87.7%; Score 493; DB 4; Length 108;  
Best Local Similarity 87.9%; Pred. No. 3e-39;  
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGDRTVITCOASODINNNYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSNLYLNWYQKPGKAPKLLIYAASLSQSGVPS 60  
  
QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGKVEIK 107  
Db 61 RFGSGSGTDFTLTISLQPEDFATYCCQYISTPLTFGGGKVEIK 107

RESULT 15  
US-09-157-370-3  
; Sequence 3, Application US/09157370A  
; Patent No. 6282238  
; GENERAL INFORMATION:  
; APPLICANT: STEIPE, Boris  
; APPLICANT: STEINBACHER, Stefan  
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES  
; FILE REFERENCE: P8341-8072  
; CURRENT APPLICATION NUMBER: US/09/157,370A  
; CURRENT FILING DATE: 1998-09-21  
; EARLIER APPLICATION NUMBER: 08/765,179  
; EARLIER FILING DATE: 1997-01-14  
; EARLIER APPLICATION NUMBER: PCT/EP95/02626  
; EARLIER FILING DATE: 1995-07-06  
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7  
; EARLIER FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-157-370-3

Query Match 86.8%; Score 488; DB 3; Length 109;  
Best Local Similarity 87.9%; Pred. No. 9e-39;  
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGDRTVITCOASODINNNYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSNLYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
  
QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGKVEIK 107  
Db 61 RFGSGSGTDFTLTISLQPEDFATYCCQYISLPTTFGGGKVEIK 107

Search completed: November 16, 2005, 22:07:21  
Job time : 19.1939 secs

THIS PAGE BLANK (CPTO)



```

US-10-330-530-26
; Sequence 26, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-26

Query Match      100.0%; Score 562; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60
DB 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60

QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
DB 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107

RESULT 3
US-10-660-357-26
; Sequence 26, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-26

Query Match      100.0%; Score 562; DB 16; Length 107;
Best Local Similarity 100.8%; Pred. No. 1.5e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60
DB 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60

QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
DB 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107

RESULT 4
US-10-727-155-318
; Sequence 318, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchko
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 318
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-318

Query Match      94.3%; Score 530; DB 17; Length 107;
Best Local Similarity 93.5%; Pred. No. 1e-39;
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60
DB 1 DIQMTQSPSSLSASVGRVTITCOASQDINNLYNWYQKPKAPKLLIYDASNLETGVP 60

QY 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107
DB 61 RFGSGSGTDFTTISGLQPEDIATYCCQYDTLPLTFGGGTKEIK 107

RESULT 5
US-10-016-986-108
; Sequence 108, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR FILING DATE: 1998-09-08
; PRIOR FILING DATE: 1997-07-24
; PRIOR FILING DATE: 1994-07-18
; PRIOR FILING DATE: 1994-01-06
; PRIOR FILING DATE: 1993-09-30
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-108

Query Match          93.4%; Score 525; DB 14; Length 107;
Best Local Similarity 94.3%; Pred. No. 2.9e-39;
Matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPR 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ELTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVPSPR 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 63 SSGSGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGTVKVEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SSGSGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGTVKVEIK 105
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
US-10-364-743-49
; Sequence 49, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 113
; TYPE: PRT
; ORGANISM: human
US-10-364-743-49

Query Match          93.1%; Score 523; DB 15; Length 113;
Best Local Similarity 93.5%; Pred. No. 4.7e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RFGSGSGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGTVKVEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 RFGSGSGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGTVKVEIK 109
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-10-452-593-49
; Sequence 49, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408

Query Match          93.1%; Score 523; DB 15; Length 113;
Best Local Similarity 93.5%; Pred. No. 4.7e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RFGSGSGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGTVKVEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 RFGSGSGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGTVKVEIK 109
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
US-10-644-277-56
; Sequence 56, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: ABGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-56

Query Match          93.1%; Score 523; DB 17; Length 152;
Best Local Similarity 92.5%; Pred. No. 6.3e-39;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNQKPGKAPKLLIYDASNLETGVP 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RFGSGSGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGTVKVEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTDTFTTISGLQPEDIATYYCQYDNLPLTFTGGGTVKVEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-10-364-743-21
; Sequence 21, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
```

```
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 164
; TYPE: PRT
; ORGANISM: human
; US-10-364-743-21

Query Match          93.1%; Score 523; DB 15; Length 164;
Best Local Similarity 93.5%; Pred. No. 6.8e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLASVSGDRVTITCOASQDINNVLNWNWYQKPGKAPKLLIYDASNLETGVPS 60
   |||||
Db 3 DIQMTSPSSLASVSGDRVTITCOASQDINNVLNWNWYQKPGKAPKLLIYDASNLETGVPS 62
   |||||

QY 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
   |||||
Db 63 RFGSGSGTDTFTTISGLQPEDIATYCCQYDNLGVTFGPTKVDIK 109
   |||||

RESULT 10
US-10-452-593-21
; Sequence 21, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 164
; TYPE: PRT
; ORGANISM: human
; US-10-452-593-21

Query Match          93.1%; Score 523; DB 16; Length 164;
Best Local Similarity 93.5%; Pred. No. 6.8e-39;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLASVSGDRVTITCOASQDINNVLNWNWYQKPGKAPKLLIYDASNLETGVPS 60
   |||||
Db 3 DIQMTSPSSLASVSGDRVTITCOASQDINNVLNWNWYQKPGKAPKLLIYDASNLETGVPS 62
   |||||

QY 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
   |||||
Db 63 RFGSGSGTDTFTTISGLQPEDIATYCCQYDNLGVTFGPTKVDIK 109
   |||||

RESULT 11
US-10-679-620-88
; Sequence 88, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hufab H2 , see Example 2
; NAME/KEY: misc feature
; LOCATION: (232)..(232)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; US-11-132-143-88

Query Match          92.7%; Score 521; DB 20; Length 502;
Best Local Similarity 92.5%; Pred. No. 3.3e-38;
Matches 99; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLASVSGDRVTITCOASQDINNVLNWNWYQKPGKAPKLLIYDASNLETGVPS 60
   |||||
Db 23 DIQMTSPSSLASVSGDRVTITCOASQDINNVLNWNWYQKPGKAPKLLIYDASNLETGVPS 82
   |||||

QY 61 RFGSGSGTDTFTTISGLQPEDIATYCCQYDTLPLTFGGTKVEIK 107
   |||||
Db 83 RFGSGSGTDTFTTISGLQPEDFATYCCQYDNLPLTFGGTKVEIK 129
   |||||

RESULT 12
US-11-132-143-88
; Sequence 88, Application US/11132143
; Publication No. US20050207977A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hufab H2 , see Example 2
; NAME/KEY: misc feature
; LOCATION: (232)..(232)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; US-11-132-143-88

Query Match          92.7%; Score 521; DB 20; Length 502;
Best Local Similarity 92.5%; Pred. No. 3.3e-38;
Matches 99; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLASVSGDRVTITCOASQDINNVLNWNWYQKPGKAPKLLIYDASNLETGVPS 60
```

```
|||||
Db 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNLYNWNTHQPGKAPKLLIYDASNLETGVPS 82
|||||
QY 61 RFGSGSGTDFTTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
|||||
Db 83 RFGSGYGTDFTTTISGLQPEDPATYYCQYDNLPLTFGGGKVEIK 129
|||||

RESULT 13
US-10-401-344-4
; Sequence 4, Application US/10401344
; Publication No. US20030194404A1
; GENERAL INFORMATION:
; APPLICANT: Schering Corporation and Abgenix, Inc.
; APPLICANT: Greenfeder, Scott
; APPLICANT: Corvalan, Jose
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COME
; FILE OF INVENTION: COMPRISING SAME
; FILE REFERENCE: LI01564W1
; CURRENT APPLICATION NUMBER: US/10/401,344
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: Signal Peptide
; LOCATION: (1)-(22)
; OTHER INFORMATION:
US-10-401-344-4

Query Match 92.2%; Score 518; DB 14; Length 236;
Best Local Similarity 93.5%; Pred. No. 2.8e-38;
Matches 100; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNWNTHQPGKAPKLLIYDASNLETGVPS 60
|||||
Db 23 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNWNTHQPGKAPKLLIYDASNLETGVPS 82
|||||
QY 61 RFGSGSGTDFTTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
|||||
Db 83 RFGSGSGTDFTTTISGLQPEDIATYYCQYDNLHPLTFGGGKVEIR 129
|||||

RESULT 14
US-10-644-277-64
; Sequence 64, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: ABGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-64

Query Match 91.6%; Score 515; DB 17; Length 214;
```

```
Best Local Similarity 90.7%; Pred. No. 4.6e-38;
Matches 97; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNWNTHQPGKAPKLLIYDASNLETGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNWNTHQPGKAPKLLIYDASNLETGVPS 60
|||||
QY 61 RFGSGSGTDFTTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
|||||
Db 61 RFGSGSGTDFTTTISGLQPEDIATYYCQYDNLITFGGTRLEIK 107
|||||

RESULT 15
US-11-031-485-132
; Sequence 132, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: MULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MadCAM
; FILE REFERENCE: ABX-PR6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 132
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-132

Query Match 91.2%; Score 512.5; DB 20; Length 107;
Best Local Similarity 92.5%; Pred. No. 3.8e-38;
Matches 99; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNWNTHQPGKAPKLLIYDASNLETGVPS 60
|||||
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINNLYNWNTHQPGKAPKLLIYDASNLETGVPS 60
|||||
QY 61 RFGSGSGTDFTTTISGLQPEDIATYYCQYDTLPLTFGGGKVEIK 107
|||||
Db 61 RFGSGSGTDFTTTISGLQPEDIATYYCQYDNLITFGGTRLEIK 106
|||||
```

Search completed: November 16, 2005, 23:05:44  
Job time : 66.6949 secs

THE MICHIGAN STATE



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-30  
Perfect score: 556  
Sequence: 1 DQMTQSPSSLSASVGRVT.....CKFSSPPTFGTKVDIS 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	107	7	ADC99801 Anti-huma
2	556	100.0	107	7	ADP05405
3	556	100.0	107	7	ADP09843 Human ant
4	520	93.5	107	8	ADP22400 Human ant
5	520	93.5	108	8	ADP46984 Murine li
6	520	93.5	242	5	AU90902 Insulin/i
7	520	93.5	245	5	AU90947 Insulin/i
8	508	91.4	107	8	ADP22358 Human ant
9	505	90.8	107	7	ADK18922 Anti-huma
10	503	90.5	108	8	ADP46980 Murine li
11	503	90.5	108	8	ADP46982 Murine li
12	503	90.5	239	5	AU90905
13	502	90.3	242	5	AU90904
14	501	90.1	107	7	ADK18799 Anti-huma
15	501	90.1	107	7	ADK18833
16	501	90.1	107	7	ADK18608 Anti-huma
17	501	90.1	107	8	ADJ57622 TNFaipha
18	501	90.1	107	8	ADJ58753 Human 2SD
19	501	90.1	107	8	ADL25434 Human mAb
20	501	90.1	244	5	ABP44153 Human Bly
21	501	90.1	244	5	ABP44250 Human Bly
22	501	90.1	244	5	ABP44071 Human Bly
23	501	90.1	244	7	ADG94898 Single ch
24	501	90.1	244	7	ADG94980 Single ch
25	501	90.1	244	7	ADG95077 Single ch

ALIGNMENTS

RESULT 1  
ADC99801

ID ADC99801 standard; protein; 107 AA.

XX ADC99801;

AC

XX 01-JAN-2004 (first entry)

XX Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 30.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
cytostatic; melanoma; oesophageal; pancreatic; Colorectal tumour;  
cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
lung cancer; human.

OS Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

PI Gudas J;

XX WPI; 2003-587113/55.

DR N-PSDB; ADC99803.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
or condition associated with expression of MUC18 in a patient, e.g.  
tumors, cancers, and other malignancies.

PS Claim 3; SEQ ID NO 30; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising  
a heavy or light chain amino acid or a heavy or light chain variable  
domain where the antibody binds to MUC18. The monoclonal antibody of the  
invention demonstrates cytostatic activity and may be useful for treating  
a disease or condition associated with the expression of MUC18 on the  
cell surface such as tumours, specifically melanoma, oesophageal,  
pancreatic or colorectal tumours, carcinomas, particularly cervical  
carcinomas and cervical intraepithelial neoplasia and cancers including  
colorectal, breast or lung cancer, as well as other malignancies. The  
current sequence is that of the anti-human MUC18 monoclonal antibody

```

CC light chain protein of the invention.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 556; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.2e-32;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY 61 RFGSGSGTDFTLTITSSLOPEDVATYYCQKFSPPPTFGPTKVDIS 107
DB 61 RFGSGSGTDFTLTITSSLOPEDVATYYCQKFSPPPTFGPTKVDIS 107

RESULT 2
ID ADD05405
AD ADD05405 standard; protein; 107 AA.
XX
AC ADD05405;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 30.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.
XX
OS Homo sapiens.
XX
PN W02003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
WPI; 2003-577496/54.
DR N-PSDB; ADD05407.
XX
XX
Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Claim 3; SEQ ID NO 30; 87pp; English.
XX
The invention relates to a novel monoclonal antibody used for inhibiting
CC tumor growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC sequence represents an anti-MUC18 antibody light chain, variable region,
CC protein of the invention.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 556; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.2e-32;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY 61 RFGSGSGTDFTLTITSSLOPEDVATYYCQKFSPPPTFGPTKVDIS 107
DB 61 RFGSGSGTDFTLTITSSLOPEDVATYYCQKFSPPPTFGPTKVDIS 107

RESULT 3
ID ADF09843
AD ADF09843 standard; protein; 107 AA.
XX
AC ADF09843;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody light chain #8.
XX
KW cell proliferation inhibition; MUC18 tumour antigen;
KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; light chain; human.
XX
OS Homo sapiens.
XX
PN W02003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
WPI; 2003-598367/56.
DR N-PSDB; ADF09845.
XX
XX
Inhibiting cell proliferation associated with expression of MUC18 tumour
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.
XX
PS Claim 3; SEQ ID NO 30; 83pp; English.
XX
The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present amino acid
CC sequence represents a light chain from an MUC18 tumour antigen-specific
CC monoclonal antibody.
XX
SQ Sequence 107 AA;

Query Match      100.0%; Score 556; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.2e-32;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY 61 RFGSGSGTDFTLTITSSLOPEDVATYYCQKFSPPPTFGPTKVDIS 107
DB 61 RFGSGSGTDFTLTITSSLOPEDVATYYCQKFSPPPTFGPTKVDIS 107

```

## RESULT 4

ADP22400  
 ID ADP22400 standard; protein; 107 AA.  
 XX  
 AC ADP22400;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human anti-TNFa antibody light chain variable region SEQ ID NO:306.  
 XX  
 KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
 KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004050683-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038281.  
 XX  
 PR 02-DEC-2002; 2002US-0430729P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang M, Lee R;  
 PI Manchulenchon K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX  
 DR WPI; 2004-480601/45.  
 XX  
 XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 PS Example 10; SEQ ID NO 306; 213pp; English.  
 XX  
 CC The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFa in a patient sample, comprising contacting with  
 CC (I), and detecting the level of binding between the antibody and TNFa in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFa induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,

CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFa  
 CC antibody light chain variable region, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 107 AA;

Query Match 93.5%; Score 520; DB 8; Length 107;  
 Best Local Similarity 94.3%; Pred No. 2,1e-29;  
 Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGVDRVITTCRASQGIIRNYLAWYQQNPQKPKLLIYGASTLQSGVPS 60

DB 1 DIQMTQSPSSLSASVGVDRVITTCRASQGIIRNYLAWYQQNPQKPKLLIYGASTLQSGVPS 60

QY 61 RFGSGSGTDFLTITSSLPEDVATYYCQKSSPFTFGPGTKVDI 106

DB 61 RFGSGSGTDFLTITSSLPEDVATYYCQKNSAPFTFGPGTKVDI 106

## RESULT 5

ADP46984

ID ADP46984 standard; protein; 108 AA.

XX

AC ADP46984;

XX

DT 09-SEP-2004 (first entry)

XX

DE Murine light chain variable anti-amphetamine antibody protein SeqID 40.

XX

KW murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine;

KW PCP; drug addiction; antiaddictive; antibody therapy.

XX

OS Mus musculus.

XX

PN WO2004050032-A2.

XX

PD 17-JUN-2004.

XX

PF 02-DEC-2003; 2003WO-US038384.

XX

PR 02-DEC-2002; 2002US-0430717P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Owens SM, Carroll FI, Abraham P, Gunnell MG, Haak-Frendscho M;

PI Feng X;

XX

DR WPI; 2004-460981/43.

XX

PT New isolated antibody or its binding fragment that binds specifically to  
 PT a drug of abuse, useful for treating a patient suffering from addiction  
 PT to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.

XX

PS Example 1; SEQ ID NO 40; 88pp; English.

XX

CC This invention relates to novel antibodies, or binding fragments thereof,  
 CC that bind directly to various drugs of abuse. Specifically, it refers to  
 CC human or chimeric monoclonal antibodies that are capable of binding to  
 CC amphetamine, methamphetamine or phencyclidine (PCP). The present  
 CC invention describes generating hybridoma cell lines that produce such  
 CC antibodies and transforming a cell with a gene encoding the antibody,  
 CC which when conjugated to a therapeutic agent, toxin or radioisotope can  
 CC be used to treat a patient suffering from a drug addiction. Accordingly,  
 CC these compositions exhibit antiaddictive activities and can be used for  
 CC antibody therapy to treat patients suffering from a drug addiction. This  
 CC polypeptide sequence is a murine light chain variable anti-amphetamine  
 CC antibody of the invention.

XX

SQ Sequence 108 AA;

Query Match 93.5%; Score 520; DB 8; Length 108;  
 Best Local Similarity 94.3%; Pred. No. 2.1e-29;  
 Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60  
 |||  
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYAASTLQSGVPS 60  
 |||

QY 61 RFGSGSGDTFTLTSSLPEDVATYVCQKFSPPFTFGPTKVDI 106  
 |||  
 DB 61 RFGSGSGDTFTLTSSLPEDVATYVCQKFSPPFTFGPTKVDI 106  
 |||

RESULT 6  
 AAU90902  
 ID AAU90902 standard; protein; 242 AA.  
 AC AAU90902;  
 XX  
 XX 18-JUN-2002 (first entry)  
 DT  
 DE Insulin/insulin-like growth factor receptor-binding peptide #2858.  
 DE  
 KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;  
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;  
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;  
 KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.  
 OS Synthetic.  
 XX  
 XX WO200172771-A2.  
 PN  
 PD 04-OCT-2001.  
 PD  
 PF 29-MAR-2000; 2000WO-US008528.  
 PF  
 PR 29-MAR-2000; 2000WO-US008528.  
 PR  
 XX (DGIB-) DGI BIOTECHNOLOGIES LLC.  
 PA (NOVO ) NOVO NORDISK AS.  
 PA  
 PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;  
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;  
 PI Hansen PH, Ravera M, Hsiao K;  
 XX WPI; 2002-025774/03.  
 DR  
 DR Modulating insulin activity in mammalian cells, for treating e.g.  
 XX diabetes and tumors, comprises using peptides that bind to insulin or  
 XX insulin-like growth factor receptors.  
 XX  
 PS Example 5; Fig 36; 390pp; English.  
 PS  
 XX The invention relates to a method of modulating insulin activity in  
 CC mammalian cells by administering a peptide that binds the insulin  
 CC receptor (IR). A composition containing a peptide, optionally expressed  
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin  
 CC agonist are useful for treating diabetes. Also, peptides that are  
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are  
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours  
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1  
 CC receptor agonists are useful for treating neurological diseases,  
 CC including stroke and diabetic neuropathy. The peptides are also useful in  
 CC screening for compounds that bind to IR or IGF-1 receptor, potential  
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or  
 CC IGF-1 receptor-binding peptides and related amino acid sequences of the  
 CC invention  
 CC  
 SQ Sequence 242 AA;

Query Match 93.5%; Score 520; DB 5; Length 242;  
 Best Local Similarity 94.3%; Pred. No. 4.2e-29;

Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60  
 |||  
 DB 136 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYAASTLQSGVPS 195  
 |||

QY 61 RFGSGSGDTFTLTSSLPEDVATYVCQKFSPPFTFGPTKVDI 106  
 |||  
 DB 196 RFGSGSGDTFTLTSSLPEDVATYVCQKFSPPFTFGPTKVDI 241  
 |||

RESULT 7  
 AAU90947  
 ID AAU90947 standard; protein; 245 AA.  
 XX  
 AC AAU90947;  
 XX  
 XX 18-JUN-2002 (first entry)  
 DT  
 DE Insulin/insulin-like growth factor receptor-binding peptide #2903.  
 DE  
 KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;  
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;  
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;  
 KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.  
 OS Synthetic.  
 XX  
 XX WO200172771-A2.  
 PN  
 PD 04-OCT-2001.  
 PD  
 PF 29-MAR-2000; 2000WO-US008528.  
 PF  
 PR 29-MAR-2000; 2000WO-US008528.  
 PR  
 XX (DGIB-) DGI BIOTECHNOLOGIES LLC.  
 PA (NOVO ) NOVO NORDISK AS.  
 PA  
 PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;  
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;  
 PI Hansen PH, Ravera M, Hsiao K;  
 XX WPI; 2002-025774/03.  
 DR  
 DR Modulating insulin activity in mammalian cells, for treating e.g.  
 XX diabetes and tumors, comprises using peptides that bind to insulin or  
 XX insulin-like growth factor receptors.  
 XX  
 PS Disclosure; Fig 57; 390pp; English.  
 PS  
 XX The invention relates to a method of modulating insulin activity in  
 CC mammalian cells by administering a peptide that binds the insulin  
 CC receptor (IR). A composition containing a peptide, optionally expressed  
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin  
 CC agonist are useful for treating diabetes. Also, peptides that are  
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are  
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours  
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1  
 CC receptor agonists are useful for treating neurological diseases,  
 CC including stroke and diabetic neuropathy. The peptides are also useful in  
 CC screening for compounds that bind to IR or IGF-1 receptor, potential  
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or  
 CC IGF-1 receptor-binding peptides and related amino acid sequences of the  
 CC invention  
 CC  
 SQ Sequence 245 AA;

Query Match 93.5%; Score 520; DB 5; Length 245;  
 Best Local Similarity 94.3%; Pred. No. 4.3e-29;  
 Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

```

Db 139 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPLKLLIYAASLTQSGVPS 198
QY 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSPPPTFGPGTKVDI 106
Db 199 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSPPPTFGPGTKVDI 244

RESULT 8
ADP22358
ID ADP22358 standard; protein; 107 AA.
AC ADP22358;
XX
XX
DT 09-SEP-2004 (first entry)
XX
XX
DE Human anti-TNFA antibody light chain variable region SEQ ID NO:264.
XX
XX
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2004050683-A2.
XX
XX
PD 17-JUN-2004.
XX
XX
PF 02-DEC-2003; 2003WO-US038281.
XX
XX
PR 02-DEC-2002; 2002US-0430729P.
XX
XX
PA (ABGE-) ABGENIX INC.
XX
XX
PI Babcock JS, Kang JS, Poord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathanasami P, Pigott C, Liang ML, Lee R;
PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
XX
DR WPI; 2004-480601/45.
DR N-PSDB; ADP22357.
XX
XX
PT New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
XX
PS Example 10; SEQ ID NO 264; 213pp; English.
XX
XX
CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFA in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFA in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFA induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,

```

```

CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFA
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 107 AA;
XX
XX
Query Match 91.4%; Score 508; DB 8; Length 107;
Best Local Similarity 91.5%; Pred. No. 1.5e-28;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPLKLLIYAASLTQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPLKLLIYAASLTQSGVPS 60
QY 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSPPPTFGPGTKVDI 106
Db 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSPPPTFGPGTKVDI 106

RESULT 9
ADK18922
ID ADK18922 standard; protein; 107 AA.
XX
XX
AC ADK18922;
XX
XX
DT 06-MAY-2004 (first entry)
XX
XX
DE Anti-human PDGF-D antibody protein related sequence #148.
XX
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003057857-A2.
XX
XX
PD 17-JUL-2003.
XX
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
XX
PR 07-JAN-2002; 2002US-00041860.
XX
XX
PA (ABGE-) ABGENIX INC.
XX
XX
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
XX
DR WPI; 2003-587119/55.
XX
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
XX
PS Disclosure; SEQ ID NO 346; 255pp; English.
XX
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when

```

```
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 107 AA;

Query Match          90.8%; Score 505; DB 7; Length 107;
Best Local Similarity 92.5%; Pred. No. 2.4e-28;
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPKGKPKLLIYAASTLQSGVPS 60

QY 61 RFSGSGSGTDFTLTISSLPQEDVATYYCOKFSSPPPTFGPTGKVDI 106
Db 61 RFSGSGSGTDFTLTISSLPQEDVATYYCOKYNSAPWTFGGTKVEI 106

RESULT 10
ADP46980
ID ADP46980 standard; protein; 108 AA.
XX
AC ADP46980;
XX
DT 09-SEP-2004 (first entry)
XX
DE Murine light chain variable anti-amphetamine antibody protein SeqID 36.
XX
KW murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine;
KW PCP; drug addiction; antiaddictive; methamphetamine; phencyclidine;
XX
OS Mus musculus.
XX
PN WO2004050032-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038384.
XX
PR 02-DEC-2002; 2002US-0430717P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Owens SM, Carroll FI, Abraham P, Gunnell MG, Haak-Frendscho M;
PI Feng X;
XX
DR WPI; 2004-460981/43.
XX
PT New isolated antibody or its binding fragment that binds specifically to
PT a drug of abuse, useful for treating a patient suffering from addiction
PT to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.
XX
PS Example 1; SEQ ID NO 36; 88pp; English.
XX
CC This invention relates to novel antibodies, or binding fragments thereof,
CC that bind directly to various drugs of abuse. Specifically, it refers to
CC human or chimeric monoclonal antibodies that are capable of binding to
CC amphetamine, methamphetamine or phencyclidine (PCP). The present
CC invention describes generating hybridoma cell lines that produce such
CC antibodies and transforming a cell with a gene encoding the antibody,
CC which when conjugated to a therapeutic agent, toxin or radioisotope can
CC be used to treat a patient suffering from a drug addiction. Accordingly,
CC these compositions exhibit antiaddictive activities and can be used for
CC antibody therapy to treat patients suffering from a drug addiction. This
CC polypeptide sequence is a murine light chain variable anti-amphetamine
CC antibody of the invention.
XX
SQ Sequence 108 AA;

Query Match          90.5%; Score 503; DB 8; Length 108;
Best Local Similarity 91.5%; Pred. No. 3.3e-28;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNDLAWYQQKPKGKPKLLIYAASTLQSGVPS 60

QY 61 RFSGSGSGTDFTLTISSLPQEDVATYYCOKFSSPPPTFGPTGKVDI 106
Db 61 RFSGSGSGTDFTLTISSLPQEDVATYYCOKYNSAPWTFGGTKVEI 106

Query Match          90.5%; Score 503; DB 8; Length 108;
Best Local Similarity 91.5%; Pred. No. 3.3e-28;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNDLAWYQQKPKGKPKLLIYAASTLQSGVPS 60

QY 61 RFSGSGSGTDFTLTISSLPQEDVATYYCOKFSSPPPTFGPTGKVDI 106
Db 61 RFSGSGSGTDFTLTISSLPQEDVATYYCOKYNSAPWTFGGTKVEI 106

RESULT 11
ADP46982
ID ADP46982 standard; protein; 108 AA.
XX
AC ADP46982;
XX
DT 09-SEP-2004 (first entry)
XX
DE Murine light chain variable anti-amphetamine antibody protein SeqID 38.
XX
KW murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine;
KW PCP; drug addiction; antiaddictive; methamphetamine; phencyclidine;
XX
OS Mus musculus.
XX
PN WO2004050032-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038384.
XX
PR 02-DEC-2002; 2002US-0430717P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Owens SM, Carroll FI, Abraham P, Gunnell MG, Haak-Frendscho M;
PI Feng X;
XX
DR WPI; 2004-460981/43.
XX
PT New isolated antibody or its binding fragment that binds specifically to
PT a drug of abuse, useful for treating a patient suffering from addiction
PT to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.
XX
PS Claim 2; SEQ ID NO 38; 88pp; English.
XX
CC This invention relates to novel antibodies, or binding fragments thereof,
CC that bind directly to various drugs of abuse. Specifically, it refers to
CC human or chimeric monoclonal antibodies that are capable of binding to
CC amphetamine, methamphetamine or phencyclidine (PCP). The present
CC invention describes generating hybridoma cell lines that produce such
CC antibodies and transforming a cell with a gene encoding the antibody,
CC which when conjugated to a therapeutic agent, toxin or radioisotope can
CC be used to treat a patient suffering from a drug addiction. Accordingly,
CC these compositions exhibit antiaddictive activities and can be used for
CC antibody therapy to treat patients suffering from a drug addiction. This
CC polypeptide sequence is a murine light chain variable anti-amphetamine
CC antibody of the invention.
XX
SQ Sequence 108 AA;

Query Match          90.5%; Score 503; DB 8; Length 108;
Best Local Similarity 91.5%; Pred. No. 3.3e-28;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNDLAWYQQKPKGKPKLLIYAASTLQSGVPS 60

QY 61 RFSGSGSGTDFTLTISSLPQEDVATYYCOKFSSPPPTFGPTGKVDI 106
Db 61 RFSGSGSGTDFTLTISSLPQEDVATYYCOKYNSAPWTFGGTKVEI 106

Query Match          90.5%; Score 503; DB 8; Length 108;
Best Local Similarity 91.5%; Pred. No. 3.3e-28;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

```
RESULT 12
AAU90905
ID AAU90905 standard; protein; 239 AA.
XX
AC AAU90905;
XX
DT 18-JUN-2002 (first entry)
XX
DE Insulin/insulin-like growth factor receptor-binding peptide #2861.
XX
KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
XX ophthalmological; insulin; receptor; gene therapy; diabetes;
XX insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
XX diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
XX
OS Synthetic.
XX
PN WO200172771-A2.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2000; 2000WO-US008528.
XX
PR 29-MAR-2000; 2000WO-US008528.
XX
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
XX (NOVO ) NOVO NORDISK AS.
XX
PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI Hansen PH, Ravera M, Hsiao K;
XX
DR WPI; 2002-025774/03.
XX
PT Modulating insulin activity in mammalian cells, for treating e.g.
PT diabetes and tumors, comprises using peptides that bind to insulin or
PT insulin-like growth factor receptors.
XX
PS Example 5; Fig 39; 390pp; English.
XX
CC The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or
CC IGF-1 receptor-binding peptides and related amino acid sequences of the
CC invention
XX
SQ Sequence 239 AA;
XX
Query Match 90.5%; Score 503; DB 5; Length 239;
Best Local Similarity 91.5%; Pred. No. 6.5e-28;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNVLAWYQKPGKPKLLIYGASTLQSGVPS 60
DB 133 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNVLAWYQKPGKPKLLIYGASTLQSGVPS 192
QY 61 RPSGSGSGTDFLTITSSLPEDVATYYCOKFSSPPFTFGGKVDI 106
DB 193 RPSGSGSGTDFLTITSSLPEDVATYYCOKYNSAPWTFQGKVEI 238
RESULT 13
AAU90904
ID AAU90904 standard; protein; 242 AA.
XX
```

```
XX
AC AAU90904;
XX
DT 18-JUN-2002 (first entry)
XX
DE Insulin/insulin-like growth factor receptor-binding peptide #2860.
XX
KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
XX ophthalmological; insulin; receptor; gene therapy; diabetes;
XX insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
XX diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
XX
OS Synthetic.
XX
PN WO200172771-A2.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2000; 2000WO-US008528.
XX
PR 29-MAR-2000; 2000WO-US008528.
XX
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
XX (NOVO ) NOVO NORDISK AS.
XX
PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI Hansen PH, Ravera M, Hsiao K;
XX
DR WPI; 2002-025774/03.
XX
PT Modulating insulin activity in mammalian cells, for treating e.g.
PT diabetes and tumors, comprises using peptides that bind to insulin or
PT insulin-like growth factor receptors.
XX
PS Example 5; Fig 38; 390pp; English.
XX
CC The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or
CC IGF-1 receptor-binding peptides and related amino acid sequences of the
CC invention
XX
SQ Sequence 242 AA;
XX
Query Match 90.3%; Score 502; DB 5; Length 242;
Best Local Similarity 90.6%; Pred. No. 7.8e-28;
Matches 96; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNVLAWYQKPGKPKLLIYGASTLQSGVPS 60
DB 136 DIQMTQSPSSLSASVGDRVTITCRASQGIIRNVLAWYQKPGKPKLLIYGASTLQSGVPS 195
QY 61 RPSGSGSGTDFLTITSSLPEDVATYYCOKFSSPPFTFGGKVDI 106
DB 196 RPSGSGSGTDFLTITSSLPEDVATYYCOKYNSAPWTFQGKLEI 241
RESULT 14
ADK18799
ID ADK18799 standard; protein; 107 AA.
XX
AC ADK18799;
XX
```

```
DT 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #25.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX OS
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 223; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 107 AA;
XX
XX Query Match 90.1%; Score 501; DB 7; Length 107;
XX Best Local Similarity 91.5%; Pred. No. 4.5e-28;
XX Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIINYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIINYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Qy 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKFSSPPFTFGPGTKVDI 106
Db 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKYNSAPLTFGGGTKEI 106

RESULT 15
ADK18833
ID ADK18833 standard; protein; 107 AA.
XX
XX AC ADK18833;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #59.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX OS
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX
```

```
PF 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 257; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 107 AA;
XX
XX Query Match 90.1%; Score 501; DB 7; Length 107;
XX Best Local Similarity 91.5%; Pred. No. 4.5e-28;
XX Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIINYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIINYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Qy 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKFSSPPFTFGPGTKVDI 106
Db 61 RFSGSGSGTDFTLTISSLPEDVATYYCOKYNSAPLTFGGGTKEI 106

Search completed: November 16, 2005, 21:51:42
Job time : 62.3676 secs
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-30  
Perfect score: 556  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQKFSPPPTFGPGTKVDIS 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	489	87.9	131	2 S40352	Ig kappa chain V-J
2	479.5	86.2	107	2 S36275	Ig lambda chain V
3	470	84.5	132	2 S40334	Ig kappa chain - h
4	463	83.3	129	2 S52792	Ig kappa chain V r
5	462	83.1	107	2 S36269	Ig lambda chain V
6	460	82.7	95	2 PH0863	Ig kappa chain V r
7	460	82.7	107	2 S40366	Ig kappa chain V-J
8	459.5	82.6	124	2 S40336	Ig kappa chain V-J
9	459	82.6	108	2 B49047	Ig kappa chain V r
10	459	82.6	127	2 S40367	Ig kappa chain V-J
11	457	82.2	123	2 S40331	Ig kappa chain - h
12	455	81.8	107	2 S36264	Ig lambda chain V
13	455	81.8	125	2 S40349	Ig kappa chain V-J
14	454.5	81.7	108	2 S30521	Ig kappa chain V r
15	454	81.7	108	1 K1HWE	Ig kappa chain V-I
16	453	81.5	125	2 S40333	Ig kappa chain V-J
17	452	81.3	117	2 S46376	Ig kappa chain V-J
18	451	81.1	108	2 S36279	Ig lambda chain V
19	451	81.1	127	2 S11240	Ig kappa chain V r
20	450	80.9	117	2 S46371	Ig kappa chain V-J
21	449	80.8	108	1 K1HUBN	Ig kappa chain V-I
22	449	80.8	110	2 S44118	Ig kappa chain V-J
23	448	80.6	107	2 S36262	Ig lambda chain V
24	448	80.6	108	2 S40330	Ig kappa chain V-J
25	448	80.6	108	2 S19674	Ig kappa chain V r
26	448	80.6	129	2 S40317	Ig kappa chain - h
27	447	80.4	108	1 K1HURE	Ig kappa chain V-I
28	447	80.4	129	2 S40369	Ig kappa chain - h
29	446	80.2	109	2 S31981	Ig kappa chain - h

30 445 80.0 128 2 S46372 Ig light chain var  
31 445 80.0 129 2 S52793 Ig kappa chain V r  
32 444.5 79.9 108 2 S34007 Ig kappa chain V r  
33 444 79.9 129 2 S52789 Ig kappa chain V r  
34 442.5 79.6 106 2 PC2397 anti-tetanus toxin  
35 441 79.3 105 2 S36266 Ig lambda chain V  
36 441 79.3 120 2 S46370 Ig kappa chain V-J  
37 440 79.1 123 2 S40313 Ig kappa chain V-J  
38 440 79.1 129 1 K1HUKW Ig kappa chain pre  
39 440 79.1 132 2 S38646 Ig kappa chain V r  
40 439.5 79.0 101 2 S44117 Ig kappa chain V-J  
41 439 79.0 108 1 K1HURY Ig kappa chain V-I  
42 439 79.0 108 1 K1HUSW Ig kappa chain V-I  
43 439 79.0 108 2 S44122 Ig kappa chain V r  
44 439 79.0 139 2 S40365 Ig kappa chain - h  
45 438 78.8 108 2 S36277 Ig lambda chain V

#### ALIGNMENTS

##### RESULT 1

S40352  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40352  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40352  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-131 <KLR>  
A:Cross-references: EMBL:X72462; NID:g441392; PIDN:CAA51130.1; PID:g441393  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 489; DB 2; Length 131;  
Best Local Similarity 89.6%; Pred No. 3e-35;  
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60  
DB 21 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQQNPGKVPKLLIYAASLTQSGVPS 80  
QY 61 RPSGSGSGTDTLTITSISSLPEDVATYYCQKFSPPPTFGPGTKVDI 106  
DB 81 RPSGSGSGTDFSLTITSISSLPEDVATYYCQKNSVPRTFGQGTKEI 126

##### RESULT 2

S36275  
Ig lambda chain V region (clone alpha-FOG1-A4) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: S36275  
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; McCafferty, J.;  
EMBO J. 12, 723-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36275  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-107 <GRI>  
A:Cross-references: EMBL:Z18827; NID:g33416; PIDN:CAA79279.1; PID:g939909  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 479.5; DB 2; Length 107;

Best Local Similarity 89.6%; Pred. No. 1.6e-34;  
Matches 95; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYAASTLQSGVPS 60

QY 61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPPTFGPGTKVDI 106  
Db 61 RFSGSGSGTDFLTITSSLOPEDVAVYYCQYVSTP-TFGGQTKVEI 105

RESULT 3  
S40334  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40334  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40334  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-132 <KLE>  
A:Cross-references: EMBL:X72444  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 470; DB 2; Length 132;  
Best Local Similarity 84.9%; Pred. No. 1.3e-33;  
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60  
Db 22 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYAASTLQSGVPS 81

QY 61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPPTFGPGTKVDI 106  
Db 82 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPPTFGGQTKVEI 127

RESULT 4  
S52792  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
C:Accession: S52792  
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,  
submitted to the EMBL Data Library, March 1995  
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-  
A:Reference number: S52789  
A:Accession: S52792  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <ROC>  
A:Cross-references: EMBL:X85986; NID:g758598; PIDN:CAA59988.1; PID:g758599  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 463; DB 2; Length 129;  
Best Local Similarity 84.9%; Pred. No. 5e-33;  
Matches 90; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60  
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYAASTLQSGVPS 82

QY 61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPPTFGPGTKVDI 106  
Db 61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPPTFGGQTKVEI 106

Db 83 RFSGSGSGADFTLTITSSLOPEDSATYYCQSYGTPTFTFGPGTKVDI 128

RESULT 5  
S36269  
Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: S36269  
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36269  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-107 <GRI>  
A:Cross-references: EMBL:Z18838; NID:g33422; PIDN:CAA79290.1; PID:g939915  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 462; DB 2; Length 107;  
Best Local Similarity 84.9%; Pred. No. 5.1e-33;  
Matches 90; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNDLGHYQKPGKAPKLLIYGTSSLQSGVPS 60

QY 61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPPTFGPGTKVDI 106  
Db 61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPPPTFGGQTKLEI 106

RESULT 6  
PH0863  
Ig kappa chain V region (anti-DNA, III-2R) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 09-Jul-2004  
C:Accession: PH0863  
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.  
J. Exp. Med. 174, 1639-1652, 1991  
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.  
A:Reference number: PH0862; MUID:92078875; PMID:1660528  
A:Accession: PH0863  
A:Molecule type: DNA  
A:Residues: 1-95 <MAN>  
A:Cross-references: UNIPROT:Q9UL70  
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-23/Region: framework 1  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:24-34/Region: complementarity-determining 1  
F:35-49/Region: framework 2  
F:50-56/Region: complementarity-determining 2  
F:57-88/Region: framework 3  
F:89-95/Region: complementarity-determining 3

Query Match 82.7%; Score 460; DB 2; Length 95;  
Best Local Similarity 93.7%; Pred. No. 6.7e-33;  
Matches 89; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYGASTLQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQQNPQKVPKLLIYAASTLQSGVPS 60

QY 61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPP 95  
Db 61 RFSGSGSGTDFLTITSSLOPEDVATYYCQKFSPP 95

```
RESULT 7
S40366
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40366
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40366
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-107 <KLE>
A:Cross-references: EMBL:X72476; NID:g441420; PIDN:CAAS1144.1; PID:g441421
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match      82.7%; Score 460; DB 2; Length 107;
Best Local Similarity 93.7%; Pred. No. 7.5e-33;
Matches 89; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
DB 13 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPGKVPKLLIYAASLQSGVPS 72

QY 61 RPSGSGSGTDFLTITSSLOPEDVATYYCQKPSPP 95
DB 73 RPSGSGSGTDFLTITSSLOPEDVATYYCQKNSAP 107

RESULT 8
S40336
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40336
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40336
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-124 <KLE>
A:Cross-references: EMBL:X72446; NID:g441360; PIDN:CAAS1114.1; PID:g441361
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match      82.6%; Score 459.5; DB 2; Length 124;
Best Local Similarity 83.2%; Pred. No. 9.6e-33;
Matches 89; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
DB 16 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPGKVPKLLIYAASLQSGVPS 75

QY 61 RPSGSGSGTDFLTITSSLOPEDVATYYCQKPS - PPFTFGPGTKVDI 106
DB 76 RPSGSGSGTDFLTITSSLOPEDVATYYCQQLNTYPPFTFGPGTKVEI 122

RESULT 9
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B49047
R:Viccor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
```

```
A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: B49047
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A:Experimental source: thymic B lymphocytes
A>Note: sequence extracted from NCB1 backbone (NCBIN:113208, NCBIP:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      82.6%; Score 459; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 9.3e-33;
Matches 90; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKLLIYAASLQSGVPS 60

QY 61 RPSGSGSGTDFLTITSSLOPEDVATYYCQKPSPPFTFGPGTKVDI 106
DB 61 RPSGSGSGTDFLTITSSLOPEDVATYYCQSYSTPLTFGGTKVEI 106

RESULT 10
S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40367
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLE>
A:Cross-references: EMBL:X72477
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match      82.6%; Score 459; DB 2; Length 127;
Best Local Similarity 84.0%; Pred. No. 1.1e-32;
Matches 89; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
DB 18 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKLLIYAASLQSGVPS 77

QY 61 RPSGSGSGTDFLTITSSLOPEDVATYYCQKPSPPFTFGPGTKVDI 106
DB 78 RPSGSGSGTDFLTITSSLOPEDVATYYCQSYNTPTTFGQGTKEI 123

RESULT 11
S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40331
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:g441350; PIDN:CAAS1109.1; PID:g441351
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 82.2%; Score 457; DB 2; Length 123;  
Best Local Similarity 84.9%; Pred. No. 1.6e-32;  
Matches 90; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60  
Db 17 DIQMTQSPSSLSASVGRVTITCRASQGISYLNWYQQKPGKAPKLLIYAASLQSGVPS 76  
QY 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPPTFGGTKVDI 106  
Db 77 RFSGSGGTDFLTITISLQPEDVATYYCQGSYSTPRTFGGTKVEI 122

#### RESULT 12

S36264  
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C;Accession: S36264  
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A;Title: Human anti-self antibodies with high specificity from phage display libraries.  
A;Reference number: S36256; MUID:93178448; PMID:7679990  
A;Accession: S36264  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-107 <GRI>  
A;Cross-references: EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID:g939919  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 455; DB 2; Length 107;  
Best Local Similarity 83.0%; Pred. No. 2e-32;  
Matches 88; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60  
Db 1 EIVLTQSPSSLSASVGRVTITCRASQGISYLNWYQQKPGKAPKLLIYAASLQSGVPS 60  
QY 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPPTFGGTKVDI 106  
Db 61 RFSGSGGTDFLTITISLQPEDVATYYCQYSNYPLTFGGTKVDI 106

#### RESULT 13

S40349  
Ig kappa chain V-J region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S40349  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40349  
A;Accession: S40349  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-125 <KLE>  
A;Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 455; DB 2; Length 125;  
Best Local Similarity 83.8%; Pred. No. 2.4e-32;  
Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSR 61  
Db 19 IQLTQSPSSLSASVGRVTITCRASQGISALAWYQQKPGKAPKLLIYDASSLESQVPSR 78

QY 62 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPPTFGGTKVDI 106  
Db 79 RFSGSGGTDFLTITISLQPEDVATYYCQFNTPYPLTFGGTKVEI 123

#### RESULT 14

S30521  
Ig kappa chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S30521  
R;Mariette, X.  
submitted to the EMBL Data Library, October 1992  
A;Reference number: S30520  
A;Accession: S30521  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-108 <MAR>  
A;Cross-references: UNIPROT:Q9UL79; EMBL:Z18327  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 454.5; DB 2; Length 108;  
Best Local Similarity 80.6%; Pred. No. 2.3e-32;  
Matches 87; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60  
Db 1 DTQLTQSPFLSASVGRVTITCRASQGISYLNWYQQKPGKAPKLLIYATSLQSGVPS 60  
QY 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPPTFGGTKVDI 107  
Db 61 RFSGSGGTDFLTITISLQPEDVATYYCOOLNSYPPTFGGTKLEIN 108

#### RESULT 15

K1HUNE  
Ig kappa chain V-I region (WEA) - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004  
C;Accession: A01876  
R;Goni, F.; Frangione, B.  
Proc. Natl. Acad. Sci. U.S.A. 80, 4937-4841, 1983  
A;Title: Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) with  
A;Reference number: A93964; MUID:83273707; PMID:6410398  
A;Accession: A01876  
A;Molecule type: protein  
A;Residues: 1-108 <GON>  
A;Cross-references: UNIPROT:P01610  
C;Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated gal

#### RESULT 16

S40349  
Ig kappa chain V-I region (WEA) - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004  
C;Accession: A01876  
R;Goni, F.; Frangione, B.  
Proc. Natl. Acad. Sci. U.S.A. 80, 4937-4841, 1983  
A;Title: Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) with  
A;Reference number: A93964; MUID:83273707; PMID:6410398  
A;Accession: A01876  
A;Molecule type: protein  
A;Residues: 1-108 <GON>  
A;Cross-references: UNIPROT:P01610  
C;Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated gal

Query Match 81.7%; Score 454; DB 1; Length 108;  
Best Local Similarity 82.1%; Pred. No. 2.5e-32;  
Matches 87; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLTWYQQKPGKAPKLLIYATSLQSGVPS 60  
QY 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPPTFGGTKVDI 106  
Db 61 RFSGSGGTDFLTITISLQPEDVATYYCQKFSPPPTFGGTKVDI 106

Db 61 RFGSGSGTEFTLTINSLOPEDFATYYCLOYSSFPWTFGQGTKEV 106

Search completed: November 16, 2005, 22:04:09  
Job time : 12.7849 secs

AMERICAN BANK (USPTO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-30  
Perfect score: 556  
Sequence: 1 DIQMTQSPSSLSASVGDRTV.....CQKFSPPFTFGPGTKVDIS 107

Scoring table: BLOSUM62  
Gapop:10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	89.6	108	2 Q9UL70	Q9ul70 homo sapien
2	480	86.3	236	2 Q6GMX8	Q6gmX8 homo sapien
3	458	82.4	236	2 Q6PIH7	Q6piH7 homo sapien
4	454	81.7	108	1 KVIK HUMAN	P01610 homo sapien
5	433	81.5	108	1 KVIY HUMAN	P80362 homo sapien
6	450	80.9	236	2 Q7Z3Y4	Q7z3Y4 homo sapien
7	449	80.8	108	2 KVIY HUMAN	P04430 homo sapien
8	448	80.6	108	2 Q9UL77	Q9ul77 homo sapien
9	447	80.4	108	1 KVIQ HUMAN	P01607 homo sapien
10	445	80.0	236	2 Q6GMW1	Q6gmW1 homo sapien
11	443.5	79.8	107	2 Q9UL81	Q9ul81 homo sapien
12	442.5	79.6	107	2 Q96SA9	Q96sa9 homo sapien
13	442	79.5	244	2 Q65ZC8	Q65zc8 homo sapien
14	440	79.1	129	1 KVIW HUMAN	P04431 homo sapien
15	439	79.0	108	1 KVIQ HUMAN	P01608 homo sapien
16	439	79.0	108	1 KVIQ HUMAN	P01609 homo sapien
17	437	78.6	108	1 KVIW HUMAN	P01605 homo sapien
18	437	78.6	240	2 Q65ZC9	Q65zc9 homo sapien
19	436.5	78.5	107	1 KVID HUMAN	P01596 homo sapien
20	436	78.4	236	2 Q6GMX0	Q6gmX0 homo sapien
21	435	78.2	108	1 KVIK HUMAN	P01597 homo sapien
22	434	78.1	108	1 KVIK HUMAN	P01594 homo sapien
23	434	78.1	108	1 KVIH HUMAN	P01599 homo sapien
24	434	78.1	108	1 KVIH HUMAN	P01611 homo sapien
25	432	77.7	108	1 KVIS HUMAN	Q9ul79 homo sapien
26	431	77.5	236	2 Q6GMX9	Q6gmX9 homo sapien
27	431	77.5	236	2 Q6PII5	Q6piI5 homo sapien
28	431	77.5	236	2 Q6PII5	Q6piI5 homo sapien
29	430	77.3	108	1 KVIU HUMAN	P01598 homo sapien
30	427	76.8	108	1 KVIK HUMAN	P01598 homo sapien
31	425	76.4	234	2 Q7Z473	Q7z473 homo sapien

32	424	76.3	108	1 KVIK HUMAN	P01593 homo sapien
33	419	75.4	129	1 KVIK HUMAN	P04432 homo sapien
34	418	75.2	108	1 KVIK HUMAN	P01603 homo sapien
35	417	75.0	236	2 Q6PIH4	Q6piH4 homo sapien
36	414	74.5	108	1 KVIC HUMAN	P01595 homo sapien
37	414	74.5	108	1 KVIN HUMAN	P01606 homo sapien
38	413	74.3	116	2 Q6PFF6	Q6pff6 homo sapien
39	412	74.1	117	1 KVIJ HUMAN	P01601 homo sapien
40	410.5	73.8	109	1 KVIJ HUMAN	P01612 homo sapien
41	407	73.2	117	1 KVIJ HUMAN	P01602 homo sapien
42	399	71.8	109	2 Q920E6	Q920e6 mus musculu
43	397	71.4	134	1 KVIC HUMAN	P06314 homo sapien
44	396	71.2	114	1 KVIC HUMAN	P01625 homo sapien
45	392	70.5	298	2 Q9QYF0	Q9qyf0 synthetic c

ALIGNMENTS

RESULT 1  
Q9UL70 PRELIMINARY; PRT; 108 AA.  
AC Q9UL70;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
DE Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035044; AAD56280.1; -.  
DR PIR; PH0863; PH0863.  
DR HSSP; P01607; IBMW.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 89.6%; Score 498; DB 2; Length 108;  
Best Local Similarity 90.6%; Pred. No. 2 8e-43;  
Matches 96; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY	1	DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQNPQPGKVPKLLIYGASTLQSGVPS 60		
Db	1	DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQNPQPGKVPKSLIYAASTLQSGVPS 60		
QY	61	RFSGSGSGTDTLTITSSLPQEDVATYCYCKFSPPFTFGPGTKVDI 106		
Db	61	RFSGSGSGTDTLTITSSLPQEDVATYCYCKYNSAPRTFGPGTKLEI 106		

RESULT 2  
Q6GMX8 PRELIMINARY; PRT; 236 AA.  
AC Q6GMX8;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Malek J.A., Casavant T.L., Scheetz T.E.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BC073764; AAH73764.1; -  
 DR HSSP; P01607; 1AR2.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003596; Ig\_MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; IGV; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG-LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;  
 Query Match 86.3%; Score 480; DB 2; Length 236;  
 Best Local Similarity 87.7%; Pred. No. 4.8e-41;  
 Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60  
 Db 23 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 82  
 QY 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSPPPTFGPGTKVDI 106  
 Db 83 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSPPPTFGPGTKVDI 128  
 RESULT 3  
 Q6PIH7 PRELIMINARY; PRT; 236 AA.  
 AC Q6PIH7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;

RN SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Malek J.A., Casavant T.L., Scheetz T.E.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RC Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034141; AAH34141.1; -  
 DR HSSP; P01607; 1AR2.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003596; Ig\_MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; IGV; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG-LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;  
 Query Match 82.4%; Score 458; DB 2; Length 236;  
 Best Local Similarity 84.0%; Pred. No. 8.7e-39;  
 Matches 89; Conservative 6; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60  
 Db 23 DIQMTQSPSSLSASVGRVTITCRASQIGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 82  
 QY 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSPPPTFGPGTKVDI 106  
 Db 83 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSPPPTFGPGTKVDI 128  
 RESULT 4  
 KVIR\_HUMAN STANDARD; PRT; 108 AA.  
 ID KVIR\_HUMAN  
 AC P01610;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-I region WEA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83273707; PubMed=6410398;



RA Goni F., Frangione B.;  
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
 RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose  
 RT in Klebsiella polysaccharides K30 and K33.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).  
 CC -!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody  
 CC against 3,4-pyruvylated galactose and isolated from a patient with  
 CC Waldenström's macroglobulinemia.

CC PIR; A01876; K1HUWE.  
 DR HSP; P80362; 1WTL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 DR Direct protein sequencing; Immunoglobulin V region;  
 KW Monoclonal antibody.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Complementarity-determining-3.  
 FT DOMAIN 98 107 Framework-4.  
 FT DISULFID 23 88 By similarity.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61P0945618C CRC64;

Query Match 81.7%; Score 454; DB 1; Length 108;  
 Best Local Similarity 82.1%; Pred. No. 9e-39;  
 Matches 87; Conservative 9; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNVLAWYQONPGKVPKLLIYGASTLQSGVPS 60  
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNVLAWYQONPGKVPKLLIYGASTLQSGVPS 60  
 QY 61 RFGSGSGGDTFTLTISLQPEVATYVCOKFSSPPPTFGPTKVDI 106  
 DB 61 RFGSGSGGDTFTLTISLQPEVATYVCOKFSSPPPTFGPTKVDI 106

RESULT 5  
 KVIY\_HUMAN STANDARD; PRT; 108 AA.  
 ID KVIY\_HUMAN STANDARD; PRT; 108 AA.  
 AC P80362;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ig kappa chain V-I region WAT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95086080; PubMed=7993911;  
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,  
 RA Solomon A., Stevens F.J., Schiffer M.;  
 RT "Comparison of crystal structures of two homologous proteins:  
 RT structural origin of altered domain interactions in immunoglobulin  
 RT light-chain dimers.";  
 RL Biochemistry 33:14848-14857 (1994).  
 RN [2]  
 RP SEQUENCE OF 1-35.  
 RX MEDLINE=81267384; PubMed=6167731;  
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,  
 RA Popp R.A., Solomon A.;  
 RT "Characterization and preliminary crystallographic data on the V-I  
 RT related fragment of the human kappa Bence Jones protein wat.";  
 RL J. Mol. Biol. 147:185-193 (1981).

CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PDB; 1WTL; X-ray; A/B=1-108.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 DR 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Complementarity-determining-3.  
 FT DOMAIN 98 107 Framework-4.  
 FT DISULFID 23 88 By similarity.  
 FT CONFLICT 30 31 TN -> SD (in Ref. 2).  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT TURN 15 16  
 FT STRAND 19 25  
 FT TURN 30 31  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 45 49  
 FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 84 90  
 FT STRAND 98 98  
 FT STRAND 102 106  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAB697 CRC64;

Query Match 81.5%; Score 453; DB 1; Length 108;  
 Best Local Similarity 80.2%; Pred. No. 1.1e-38;  
 Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNVLAWYQONPGKVPKLLIYGASTLQSGVPS 60  
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQIGIRNVLAWYQONPGKVPKLLIYGASTLQSGVPS 60  
 QY 61 RFGSGSGGDTFTLTISLQPEVATYVCOKFSSPPPTFGPTKVDI 106  
 DB 61 RFGSGSGGDTFTLTISLQPEVATYVCOKFSSPPPTFGPTKVDI 106

RESULT 6  
 Q723Y4 PRELIMINARY; PRT; 236 AA.  
 ID Q723Y4 PRELIMINARY; PRT; 236 AA.  
 AC Q723Y4; (Tremblrel. 25, Created)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-NAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal Muscle;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,



Db 61 RPSGSGTGDTFTLTSSLPQDPFATYYCQOYSTSWTFGEGTKVEI 106

RESULT 9

KVIO\_HUMAN STANDARD; PRT; 108 AA.

AC P01607;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Ig kappa chain V-I region Rei.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RN SEQUENCE

RP MEDLINE=76023758; PubMed=809329;

RA Palm W., Hilschmann N.;

RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";

RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=76039968; PubMed=1182131;

RA Epp O., Latman E.E., Schiffer M., Huber R., Palm W.;

RT "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Rei refined at 2.0-A resolution.";

RL Biochemistry 14:4943-4952(1975).

CC - MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.

CC - MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A91663; KIHURE.

DR PDB; 1AR2; X-ray; @=1-107.

DR PDB; 1BWV; X-ray; A/B=1-107.

DR PDB; 1REI; X-ray; A/B=1-107.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-like.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG\_LIKE; 1.

KW 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.

FT DOMAIN 24 34 Complementarity-determining-1.

FT DOMAIN 35 49 Framework-2.

FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.

FT DOMAIN 89 97 Complementarity-determining-3.

FT DOMAIN 98 107 Framework-4.

FT DISULFID 23 88

FT STRAND 4 7

FT STRAND 10 13

FT TURN 15 16

FT STRAND 19 25

FT TURN 30 31

FT STRAND 33 38

FT TURN 40 41

FT STRAND 45 49

FT TURN 50 52

FT STRAND 53 54

FT TURN 56 57

FT STRAND 60 61

FT TURN 62 67

FT STRAND 69 70

FT TURN 70 75

FT STRAND 80 82

FT STRAND 84 90

FT STRAND 97 98

FT STRAND 102 106

FT NON\_TER 108 108

SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 80.4%; Score 447; DB 1; Length 108;

Best Local Similarity 79.4%; Pred. No. 4.7e-38;

Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGDRVTITCRASQIGIRNVLANYQNPQGVKLLIYGASTLQSGVPS 60

DB 1 DIQMTQSPSSLSASVGDRVTITCRASQIGIRNVLANYQNPQGVKLLIYGASTLQSGVPS 60

OY 61 RPSGSGTGDTFTLTSSLPQDPFATYYCQOYSTSWTFGEGTKVEI 107

DB 61 RPSGSGTGDTFTLTSSLPQDPFATYYCQOYSTSWTFGEGTKVEI 107

RESULT 10

O6GMW1 PRELIMINARY; PRT; 236 AA.

ID O6GMW1

AC O6GMW1

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE-Spleen.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RN SEQUENCE FROM N.A.

RC TISSUE-Spleen;

RA Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073791; AAH73791.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR Pfam; PF07654; C1-set; 1.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG\_LIKE; 2.

```
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 236 AA; 25751 MW; 5BF56A087AFAC437 CRC64;

Query Match 80.0%; Score 445; DB 2; Length 236;
Best Local Similarity 83.0%; Pred. No. 1.9e-37;
Matches 88; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 2 IQWTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPKVPKLLIYGASTLQSGVPSR 61
DB 24 IQWTQSPSSLSASVGDRTVITCRASQISNDLGMVQKPKGAPKLLIYAASSLQSGVPSR 83

QY 62 FSGSGSGTDFTLTISSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106
DB 84 FSGSGSGTDFTLTISSLOPEDFATYYCLQDYNYPWTFGGGTKVEI 128

RESULT 11
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
WT Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; IBWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 79.8%; Score 443.5; DB 2; Length 107;
Best Local Similarity 84.0%; Pred. No. 1.1e-37;
Matches 89; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 1 DIQWTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPKVPKLLIYGASTLQSGVPS 60
DB 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLWYQKPKGAPNLLIYAASSLQSGVPS 60

QY 61 RFGSGSGTDFTLTISSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106
DB 61 RFGSGSGTDFTLTISSLOAEDFATYYCQ-SYSALTFFGGTKVDI 105

RESULT 12
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
WT Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 79.5%; Score 442; DB 2; Length 244;
Best Local Similarity 78.3%; Pred. No. 4e-37;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
WT Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR FIR; B49047; B49047.
DR FIR; PH0867; PH0867.
DR FIR; S16840; S16840.
DR FIR; S31977; S31977.
DR FIR; S34083; S34083.
DR FIR; S34086; S34086.
DR HSSP; P01607; IBWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 79.6%; Score 442.5; DB 2; Length 107;
Best Local Similarity 84.0%; Pred. No. 1.4e-37;
Matches 89; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIQWTQSPSSLSASVGDRTVITCRASQIGIRNYLAWYQONPKVPKLLIYGASTLQSGVPS 60
DB 1 DIQWTQSPSSLSASVGDRTVITCRASQISNYLWYQKPKGAPKLLIYAASSLQSGVPS 60

QY 61 RFGSGSGTDFTLTISSLOPEDVATYYCQKFSPPFTFGPGTKVDI 106
DB 61 RFGSGSGTDFTLTISSLOPEDFATYYCQ-SYSTLTFFGGTKVEI 105

RESULT 13
Q65ZC8 PRELIMINARY; PRT; 244 AA.
AC Q65ZC8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scfv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
WT Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 79.5%; Score 442; DB 2; Length 244;
Best Local Similarity 78.3%; Pred. No. 4e-37;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 137 DIQMTQSPSTLSASIGDRVTITTCRASEGIYHLWAWYQKPGKAPKPLIYKASSLASGAPS 196
QY 61 RFGSGSGTDFLTITSSLPQEDVATYVCQKFSPPFTFGPGTKVDI 106
Db 197 RFGSGSGTDFLTITSSLPQDFAFYCCQYQSNYPLTFGGGKLEI 242

RESULT 14
ID KVIW HUMAN STANDARD; PRT; 129 AA.
AC P0431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combricio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 Ig kappa chain V-I region Walker.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Framework-3.
FT DOMAIN 79 110 Complementarity-determining-2.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; P941FA07D4AFC9F9 CRC64;

Query Match 79.1%; Score 440; DB 1; Length 129;
Best Local Similarity 82.1%; Pred. No. 3e-37;
Matches 87; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQISNYLWYQKPGKAPKPLIYAASSLQSGVTS 82
QY 61 RFGSGSGTDFLTITSSLPQEDVATYVCQKFSPPFTFGPGTKVDI 106
Db 83 RFGSGSGTDFLTITSSLPQEDSATYCCQYSYSLTITFGGKTRLEI 128
```

```
RESULT 15
ID KVIP HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967)).
RL Cum.);";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
RL York (1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A91638; KIHURY.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; FSACEDE5A313DF3A CRC64;

Query Match 79.0%; Score 439; DB 1; Length 108;
Best Local Similarity 80.0%; Pred. No. 3.1e-37;
Matches 84; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQIGIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQISFLNLYQKPGKAPKPLIYDASKLEAGVPS 60
QY 61 RFGSGSGTDFLTITSSLPQEDVATYVCQKFSPPFTFGPGTKVD 105
Db 61 RFGSGSGTDFLTITSSLPQEDVATYVCQFDNLPLTFGGGKVD 105

Search completed: November 16, 2005, 22:01:54
Job time : 60.9908 secs
```

THE BIBLE IN THE MIDDLE

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357A-30  
Perfect score: 556  
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....CQKFSPPFTFGPGTKVDIS 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/aaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/aaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/aaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/aaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/aaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	90.1	107	3	US-08-599-226-9
2	501	90.1	107	3	US-09-125-098-9
3	501	90.1	107	4	US-09-540-018-9
4	499	89.7	107	3	US-08-599-226-1
5	499	89.7	107	3	US-09-125-098-1
6	499	89.7	107	4	US-09-540-018-1
7	483	86.9	107	1	US-08-276-852-84
8	483	86.9	107	1	US-08-899-575-84
9	483	86.9	107	5	PCT-US95-08743-84
10	483	86.9	107	5	PCT-US95-08743-84
11	480	86.3	214	4	US-09-472-087-71
12	475	85.4	106	1	US-08-276-852-83
13	475	85.4	106	1	US-08-899-575-83
14	475	85.4	106	1	US-08-899-575-83
15	475	85.4	106	5	PCT-US95-08743-83
16	475	85.4	107	1	US-08-276-852-82
17	475	85.4	107	1	US-08-899-575-82
18	475	85.4	107	1	US-08-899-575-82
19	475	85.4	107	2	US-07-934-373C-18
20	475	85.4	107	3	US-08-437-642B-18
21	475	85.4	107	4	US-08-146-206C-18
22	475	85.4	107	4	US-09-648-067A-14
23	475	85.4	107	4	US-09-705-686-18
24	475	85.4	107	4	US-09-705-392A-18
25	475	85.4	107	4	US-09-705-398-18
26	475	85.4	107	5	PCT-US93-07832-18
27	475	85.4	107	5	PCT-US95-08743-82

28 475 85.4 108 3 US-08-974-899-3 Sequence 3, Appli  
29 475 85.4 108 4 US-09-795-798-3 Sequence 3, Appli  
30 473.5 85.2 108 3 US-09-240-274-177 Sequence 177, App  
31 470 84.5 109 2 US-07-934-373C-3 Sequence 3, Appli  
32 470 84.5 109 3 US-08-437-642B-3 Sequence 3, Appli  
33 470 84.5 109 4 US-08-146-206C-3 Sequence 3, Appli  
34 470 84.5 109 4 US-09-705-686-3 Sequence 3, Appli  
35 470 84.5 109 4 US-09-705-392A-3 Sequence 3, Appli  
36 470 84.5 109 4 US-09-705-398-3 Sequence 3, Appli  
37 470 84.5 109 5 PCT-US93-07832-3 Sequence 85, Appl  
38 469 84.4 106 1 US-08-276-852-85 Sequence 85, Appl  
39 469 84.4 106 1 US-08-899-575-85 Sequence 85, Appl  
40 469 84.4 106 1 US-08-899-575-85 Sequence 85, Appl  
41 469 84.4 106 5 PCT-US95-08743-85 Sequence 85, Appl  
42 469 84.4 108 3 US-09-025-769B-14 Sequence 14, Appl  
43 469 84.4 108 4 US-09-490-070A-14 Sequence 14, Appl  
44 469 84.4 108 4 US-09-490-153-14 Sequence 14, Appl  
45 469 84.4 108 4 US-09-490-324-14 Sequence 14, Appl

## ALIGNMENTS

RESULT 1  
US-08-599-226-9  
; Sequence 9, Application US/08599226  
; Patent No. 6090382  
; GENERAL INFORMATION:  
; APPLICANT: Salfeld, Jochen G.  
; APPLICANT: Allen, Deborah J.  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Kaymakcalan, Zehra  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Mankovich, John A.  
; APPLICANT: McGuinness, Brian T.  
; APPLICANT: Roberts, Andrew J.  
; APPLICANT: Sakorafas, Paul  
; APPLICANT: Schoenhaut, David  
; APPLICANT: Vaughan, Tristan J.  
; APPLICANT: White, Michael  
; APPLICANT: Wilton, Andrew J.  
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/599,226  
; FILING DATE: 08-FEB-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A., Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal

US-08-599-226-9

Query Match 90.1%; Score 501; DB 3; Length 107;  
Best Local Similarity 89.6%; Pred. No. 5.9e-37;  
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVGRVTITCRASQGINRYLAWYQONPGKVPKLLIYGASTLQSGVPS 60  
Db 1 DIQMTQSPSLSASIGDRVTITCRASQGINRYLAWYQONPGKVPKLLIYAASTLQSGVPS 60  
QY 61 RFGSGSGTDFLTITSSLPQEDVATYYCQKFSPPFTFGTGKVDI 106  
Db 61 RFGSGSGTDFLTITSSLPQEDVATYYCQKFSPPFTFGTGKVDI 106

RESULT 2

US-09-125-098-9  
; Sequence 9, Application US/09125098  
; Patent No. 6258562  
; GENERAL INFORMATION:  
; APPLICANT: Salfeld, Jochen G.  
; APPLICANT: Allen, Deborah J.  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Kaymakalan, Zehra  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Mankovich, John A.  
; APPLICANT: McGuinness, Brian T.  
; APPLICANT: Roberts, Andrew J.  
; APPLICANT: Sakorafas, Paul  
; APPLICANT: Schoenhaut, David  
; APPLICANT: Vaughan, Tristan J.  
; APPLICANT: White, Michael  
; APPLICANT: Wilton, Andrew J.  
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/125,098  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/599,226  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A., Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-09-125-098-9

Query Match 90.1%; Score 501; DB 3; Length 107;  
Best Local Similarity 89.6%; Pred. No. 5.9e-37;  
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVGRVTITCRASQGINRYLAWYQONPGKVPKLLIYGASTLQSGVPS 60  
Db 1 DIQMTQSPSLSASIGDRVTITCRASQGINRYLAWYQONPGKVPKLLIYAASTLQSGVPS 60  
QY 61 RFGSGSGTDFLTITSSLPQEDVATYYCQKFSPPFTFGTGKVDI 106  
Db 61 RFGSGSGTDFLTITSSLPQEDVATYYCQKFSPPFTFGTGKVDI 106

RESULT 3

US-09-540-018-9  
; Sequence 9, Application US/09540018  
; Patent No. 6509015  
; GENERAL INFORMATION:  
; APPLICANT: Salfeld, Jochen G.  
; APPLICANT: Allen, Deborah J.  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Kaymakalan, Zehra  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Mankovich, John A.  
; APPLICANT: McGuinness, Brian T.  
; APPLICANT: Roberts, Andrew J.  
; APPLICANT: Sakorafas, Paul  
; APPLICANT: Schoenhaut, David  
; APPLICANT: Vaughan, Tristan J.  
; APPLICANT: White, Michael  
; APPLICANT: Wilton, Andrew J.  
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/540,018  
; FILING DATE: 31-MARCH-2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/599,226  
; FILING DATE: 08-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A., Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-09-540-018-9

Query Match 90.1%; Score 501; DB 4; Length 107;  
Best Local Similarity 89.6%; Pred. No. 5.9e-37;  
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVGRVTITCRASQGINRYLAWYQONPGKVPKLLIYGASTLQSGVPS 60  
Db 1 DIQMTQSPSLSASIGDRVTITCRASQGINRYLAWYQONPGKVPKLLIYAASTLQSGVPS 60



QY 61 RFGSGSGTDTLTITSSLOPEDVATYYCQKPSPPFTFGPGTKVDI 106  
Db 61 RFGSGSGTDTLTITSSLOPEDVATYYCQKNSAPYAFGQGTKVEI 106

## RESULT 4

US-08-599-226-1  
; Sequence 1, Application US/08599226  
; Patent No. 6090382  
; GENERAL INFORMATION:  
; APPLICANT: Salfeld, Jochen G.  
; APPLICANT: Allen, Deborah J.  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Kaymakalan, Zehra  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Mankovich, John A.  
; APPLICANT: McGuinness, Brian T.  
; APPLICANT: Roberts, Andrew J.  
; APPLICANT: Sakorafas, Paul  
; APPLICANT: Schoenhaut, David  
; APPLICANT: Vaughan, Tristan J.  
; APPLICANT: White, Michael  
; APPLICANT: Wilton, Andrew J.  
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 08-FEB-1996  
; APPLICATION NUMBER: US/08/599,226  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A., Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-599-226-1

Query Match 89.7%; Score 499; DB 3; Length 107;  
Best Local Similarity 89.6%; Pred. No. 8.8e-37;  
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGKPKLLIYGASTLQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQKPKGKAPKLLIYAASTLQSGVPS 60

QY 61 RFGSGSGTDTLTITSSLOPEDVATYYCQKPSPPFTFGPGTKVDI 106  
Db 61 RFGSGSGTDTLTITSSLOPEDVATYYCQRYNRAPYTFGQGTKVEI 106

## RESULT 5

US-09-125-098-1  
; Sequence 1, Application US/09125098

; Patent No. 6258562  
; GENERAL INFORMATION:  
; APPLICANT: Salfeld, Jochen G.  
; APPLICANT: Allen, Deborah J.  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Kaymakalan, Zehra  
; APPLICANT: Labkovsky, Boris  
; APPLICANT: Mankovich, John A.  
; APPLICANT: McGuinness, Brian T.  
; APPLICANT: Roberts, Andrew J.  
; APPLICANT: Sakorafas, Paul  
; APPLICANT: Schoenhaut, David  
; APPLICANT: Vaughan, Tristan J.  
; APPLICANT: White, Michael  
; APPLICANT: Wilton, Andrew J.  
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/125,098  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/599,226  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A., Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-09-125-098-1

Query Match 89.7%; Score 499; DB 3; Length 107;  
Best Local Similarity 89.6%; Pred. No. 8.8e-37;  
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQNPGKPKLLIYGASTLQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQQKPKGKAPKLLIYAASTLQSGVPS 60

QY 61 RFGSGSGTDTLTITSSLOPEDVATYYCQKPSPPFTFGPGTKVDI 106  
Db 61 RFGSGSGTDTLTITSSLOPEDVATYYCQRYNRAPYTFGQGTKVEI 106

## RESULT 6

US-09-540-018-1  
; Sequence 1, Application US/09540018  
; Patent No. 6509015  
; GENERAL INFORMATION:  
; APPLICANT: Salfeld, Jochen G.  
; APPLICANT: Allen, Deborah J.  
; APPLICANT: Hoogenboom, Hendricus R.J.M.

```

; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/540,018
; FILING DATE: 31-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-540-018-1

Query Match 89.7%; Score 499; DB 4; Length 107;
Best Local Similarity 89.6%; Pred. No. 8.8e-37;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DQMTQSPSSLSASVGRVTITCRASQGINRYLAWYQONPKVPKLLIYGASTLQSGVPS 60
Db 1 DQMTQSPSSLSASVGRVTITCRASQGINRYLAWYQONPKVPKLLIYGASTLQSGVPS 60

QY 61 RSGSGSGDTFTLTISLQPEDVATYYCQKFSPPFTFGPTKVDI 106
Db 61 RSGSGSGDTFTLTISLQPEDVATYYCQINRNPITFGQTKVEI 106

RESULT 7
US-08-276-852-84
; Sequence 84, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ;
```

```

; ADDRESS: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-84

Query Match 86.9%; Score 483; DB 1; Length 107;
Best Local Similarity 89.4%; Pred. No. 2.2e-35;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGRVTITCRASQGINRYLAWYQONPKVPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASVGRVTITCRASQGINRYLAWYQONPKVPKLLIYAASLTQSGVPSRF 60

QY 63 SGSGSGDTFTLTISLQPEDVATYYCQKFSPPFTFGPTKVDI 106
Db 61 SGSGSGDTFTLTISLQPEDVATYYCQKFSPPFTFGPTKVDI 106

RESULT 8
US-08-899-575-84
; Sequence 84, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; ;
```

```
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US 08/899,575
/ APPLICATION DATA:
/ FILING DATE: 24-JUL-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/276,852
/ FILING DATE: 18-JUL-1994
/ APPLICATION NUMBER: US 08/178,302
/ FILING DATE: 30-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/954,148
/ FILING DATE: 30-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCR1452P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-899-575-84

Query Match      86.9%; Score 483; DB 1; Length 107;
Best Local Similarity 89.4%; Pred. No. 2.2e-35;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPKGKPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASVGRVTITCRASQGISNYLAWYQKPKGKPKLLIYAASTLQSGVPSRF 60

QY 63 SGSGSGTDTLTITSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SGSGSGTDTLTITSSLPQEDVATYYCQKNSAPRTFGQGTKEI 104

RESULT 9
US-08-899-575-84
/ Sequence 84, Application US/08899575
/ Patent No. 5804440
/ GENERAL INFORMATION:
/ APPLICANT: Burton, Dennis R
/ APPLICANT: Barbas, Carlos F
/ APPLICANT: Lerner, Richard A
/ TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
/ TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
/ NUMBER OF SEQUENCES: 170
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: The Scripps Research Institute, Office of
/ ADDRESSEE: Patent Counsel
/ STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
/ STREET: Mail Drop TPC8
/ CITY: La Jolla
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/899,575
/ FILING DATE: 24-JUL-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/276,852
```

```
/ FILING DATE: 18-JUL-1994
/ APPLICATION NUMBER: US 08/178,302
/ FILING DATE: 30-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/954,148
/ FILING DATE: 30-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCR1452P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-899-575-84

Query Match      86.9%; Score 483; DB 1; Length 107;
Best Local Similarity 89.4%; Pred. No. 2.2e-35;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPKGKPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASVGRVTITCRASQGISNYLAWYQKPKGKPKLLIYAASTLQSGVPSRF 60

QY 63 SGSGSGTDTLTITSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SGSGSGTDTLTITSSLPQEDVATYYCQKNSAPRTFGQGTKEI 104

RESULT 10
PCT-US95-08743-84
/ Sequence 84, Application PC/TUS9508743
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
/ TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
/ NUMBER OF SEQUENCES: 170
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/08743
/ FILING DATE: 11-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/276,852
/ FILING DATE: 18-JUL-1994
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-08743-84

Query Match      86.9%; Score 483; DB 5; Length 107;
Best Local Similarity 89.4%; Pred. No. 2.2e-35;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGRVTITCRASQGIIRNYLAWYQONPKGKPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASVGRVTITCRASQGISNYLAWYQKPKGKPKLLIYAASTLQSGVPSRF 60

QY 63 SGSGSGTDTLTITSSLPQEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SGSGSGTDTLTITSSLPQEDVATYYCQKNSAPRTFGQGTKEI 104
```

```

RESULT 11
US-09-472-087-71
; Sequence 71, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 71
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-71

Query Match      86.3%; Score 480; DB 4; Length 214;
Best Local Similarity 86.8%; Pred. No. 8.1e-35;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTVTTCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db 1 DIQWTSPPSSLSASVGDRTVTTCRASQSIINSYLDWYQOKPKAPKLLIYAASLQSGVPS 60

Qy 61 RFSGSGGTDTFTLTISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 RFSGSGGTDTFTLTISLQPEDVATYYCQYVSTPFTFGPGTKVEI 106

RESULT 12
US-08-276-852-83
; Sequence 83, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937

RESULT 13
US-08-899-575-83
; Sequence 83, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937

```

```

; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-83

Query Match      85.4%; Score 475; DB 1; Length 106;
Best Local Similarity 86.5%; Pred. No. 1.1e-34;
Matches 90; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASIGDRVTITCRASQGINNLYLAWYQORPGKVPRLIIYAAASTLQSGVPTRF 60

QY 63 SSGSGGTDFTLTISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SSGSGGTDFTLTISLQPEDVATYYCQKNSVPRTFGGGKVEI 104

RESULT 14
US-08-899-575-83
; Sequence 83, Application US/08899575
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-83

Query Match      85.4%; Score 475; DB 1; Length 106;
Best Local Similarity 86.5%; Pred. No. 1.1e-34;
Matches 90; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASIGDRVTITCRASQGINNLYLAWYQORPGKVPRLIIYAAASTLQSGVPTRF 60

QY 63 SSGSGGTDFTLTISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SSGSGGTDFTLTISLQPEDVATYYCQKNSVPRTFGGGKVEI 104

RESULT 15
PCT-US95-08743-83
; Sequence 83, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08743-83

Query Match      85.4%; Score 475; DB 5; Length 106;
Best Local Similarity 86.5%; Pred. No. 1.1e-34;
Matches 90; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 3 QMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPSRF 62
Db 1 ELTQSPSSLSASIGDRVTITCRASQGINNLYLAWYQORPGKVPRLIIYAAASTLQSGVPTRF 60

QY 63 SSGSGGTDFTLTISLQPEDVATYYCQKFSPPFTFGPGTKVDI 106
Db 61 SSGSGGTDFTLTISLQPEDVATYYCQKNSVPRTFGGGKVEI 104

Search completed: November 16, 2005, 22:07:21
Job time : 18.1939 secs
```

THIS PAGE BLANK (PHOTO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds  
(without alignments)  
681.481 Million cell updates/sec

Title: US-10-660-357A-30  
Perfect score: 556  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQKFSPPPTFGTKVDIS 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications\_AA.\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	107	14	US-10-330-613-30
2	556	100.0	107	14	US-10-330-530-30
3	556	100.0	107	16	US-10-660-357-30
4	520	93.5	107	17	US-10-727-155-306
5	520	93.5	108	17	US-10-725-962-40
6	508	91.4	107	17	US-10-727-155-264
7	505	90.8	107	15	US-10-041-860-346
8	503	90.5	107	15	US-10-309-762-86
9	503	90.5	108	17	US-10-725-962-36
10	503	90.5	108	17	US-10-725-962-38
11	501	90.1	107	10	US-09-801-185A-9
Sequence 30, Appl					
Sequence 30, Appl					
Sequence 30, Appl					
Sequence 306, Appl					
Sequence 40, Appl					
Sequence 264, Appl					
Sequence 346, Appl					
Sequence 86, Appl					
Sequence 36, Appl					
Sequence 38, Appl					
Sequence 9, Appl					

12	501	90.1	107	14	US-10-041-860-32	Sequence 32, Appl
13	501	90.1	107	14	US-10-041-860-223	Sequence 223, App
14	501	90.1	107	14	US-10-041-860-257	Sequence 257, App
15	501	90.1	107	15	US-10-133-715-9	Sequence 9, Appl
16	501	90.1	107	15	US-10-302-356A-9	Sequence 9, Appl
17	501	90.1	107	15	US-10-163-657A-9	Sequence 9, Appl
18	501	90.1	107	15	US-10-422-287-9	Sequence 9, Appl
19	501	90.1	107	16	US-10-622-932-9	Sequence 9, Appl
20	501	90.1	107	16	US-10-623-065-9	Sequence 9, Appl
21	501	90.1	107	16	US-10-623-076-9	Sequence 9, Appl
22	501	90.1	107	16	US-10-622-210-9	Sequence 9, Appl
23	501	90.1	107	16	US-10-623-035-9	Sequence 9, Appl
24	501	90.1	107	16	US-10-623-075-9	Sequence 9, Appl
25	501	90.1	107	16	US-10-665-383-44	Sequence 44, Appl
26	501	90.1	107	16	US-10-622-928-9	Sequence 9, Appl
27	501	90.1	107	16	US-10-622-205-9	Sequence 82, Appl
28	501	90.1	244	10	US-09-880-748-82	Sequence 164, App
29	501	90.1	244	10	US-09-880-748-164	Sequence 261, App
30	501	90.1	244	10	US-09-880-748-461	Sequence 82, Appl
31	501	90.1	244	15	US-10-293-418-82	Sequence 164, App
32	501	90.1	244	15	US-10-293-418-164	Sequence 261, App
33	501	90.1	244	15	US-10-293-418-361	Sequence 41, Appl
34	500	89.9	108	17	US-10-725-962-41	Sequence 1, Appl
35	499	89.7	107	10	US-09-801-185A-1	Sequence 39, Appl
36	499	89.7	107	14	US-10-041-860-39	Sequence 222, App
37	499	89.7	107	14	US-10-041-860-222	Sequence 256, App
38	499	89.7	107	15	US-10-133-715-1	Sequence 1, Appl
39	499	89.7	107	15	US-10-302-356A-1	Sequence 1, Appl
40	499	89.7	107	15	US-10-163-657A-1	Sequence 1, Appl
41	499	89.7	107	15	US-10-422-287-1	Sequence 1, Appl
42	499	89.7	107	16	US-10-622-932-1	Sequence 1, Appl
43	499	89.7	107	16	US-10-623-065-1	Sequence 1, Appl
44	499	89.7	107	16	US-10-623-076-1	Sequence 1, Appl
45	499	89.7	107	16	US-10-623-076-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-30  
; Sequence 30, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ARGENIX 022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-30

Query Match 100.0%; Score 556; DB 14; Length 107;  
Best Local Similarity 100.0%; Pred. No. 3.7e-39;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DIQMTQSPSSLSASVGRVTITCRASQGI	RVNLA	WYQNP	GVKPK	LLIYG	ASTLQ	SGVPS	60
Db	1	DIQMTQSPSSLSASVGRVTITCRASQGI	RVNLA	WYQNP	GVKPK	LLIYG	ASTLQ	SGVPS	60
Qy	61	RFGSGSGTDFLTITSSLPEDVATYYCQKFS	PPPTFG	TKVDIS	107				
Db	61	RFGSGSGTDFLTITSSLPEDVATYYCQKFS	PPPTFG	TKVDIS	107				

RESULT 2

```
US-10-330-530-30
; Sequence 30, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-30

Query Match          100.0%; Score 556; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db      1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY      61 RFGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPGTKVDIS 107
Db      61 RFGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPGTKVDIS 107

RESULT 3
US-10-660-357-30
; Sequence 30, Application US/10660357
; Publication No. US2040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-30

Query Match          100.0%; Score 556; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db      1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY      61 RFGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPGTKVDIS 107
Db      61 RFGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPGTKVDIS 107

RESULT 4
US-10-727-155-306
; Sequence 306, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
```

```
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchro
; APPLICANT: Raffaela Faggioni
; APPLICANT: Raffaele Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-306

Query Match          93.5%; Score 520; DB 17; Length 107;
Best Local Similarity 94.3%; Pred. No. 3.9e-36;
Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db      1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60

QY      61 RFGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPGTKVDI 106
Db      61 RFGSGSGTDFTLTISSLPQEDVATYYCQKFSPPPTFGPGTKVDI 106

RESULT 5
US-10-725-962-40
; Sequence 40, Application US/10725962
; Publication No. US20050013809A1
; GENERAL INFORMATION:
; APPLICANT: Samuel M. Owens
; APPLICANT: Frank I. Carroll
; APPLICANT: Philip Abraham
; APPLICANT: Melinda G. Gunnell
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Xiao Feng
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; FILE REFERENCE: ABGENIX.071A
; CURRENT APPLICATION NUMBER: US/10/725,962
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-725-962-40

Query Match          93.5%; Score 520; DB 17; Length 108;
Best Local Similarity 94.3%; Pred. No. 3.9e-36;
Matches 100; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
Db      1 DIQMTQSPSSLSASVGDRTVITCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
```



Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNVLAWYQKPGKPKLLIYAASTLQSGVPS 60  
QY 61 RPSGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106  
|||||  
Db 61 RPSGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106  
|||||

## RESULT 6

US-10-727-155-264  
; Sequence 264, Application US/10727155  
; Publication No. US20050049402A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaspal S. Kang  
; APPLICANT: Orit Fiodt  
; APPLICANT: Larry Green  
; APPLICANT: Xiao Feng  
; APPLICANT: Scott Klakamp  
; APPLICANT: Mary Haak-Frendscho  
; APPLICANT: Palaniswami Rathanaswami  
; APPLICANT: Craig Pigott  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Manchulenko  
; APPLICANT: Raffaella Faggoni  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Qiaojuan Jane Su  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
; FILE REFERENCE: ABGENIX.073A  
; CURRENT APPLICATION NUMBER: US/10/727,155  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: 60/430729  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 320  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 264  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-727-155-264

Query Match 91.4%; Score 508; DB 17; Length 107;  
Best Local Similarity 91.5%; Pred. No. 3,9e-35;  
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNVLAWYQKPGKPKLLIYGASTLQSGVPS 60  
|||||  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNVLAWYQKPGKPKLLIYAASTLQSGVPS 60  
|||||  
QY 61 RPSGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106  
|||||  
Db 61 RPSGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106  
|||||

## RESULT 7

US-10-041-860-346  
; Sequence 346, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES  
; FILE REFERENCE: ABGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 346  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-346

Query Match 90.8%; Score 505; DB 14; Length 107;  
Best Local Similarity 92.5%; Pred. No. 7e-35;  
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNVLAWYQKPGKPKLLIYGASTLQSGVPS 60  
|||||  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNVLAWYQKPGKPKLLIYAASTLQSGVPS 60  
|||||  
QY 61 RPSGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106  
|||||  
Db 61 RPSGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106  
|||||

## RESULT 8

US-10-309-762-86  
; Sequence 86, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-86

Query Match 90.5%; Score 503; DB 15; Length 107;  
Best Local Similarity 91.5%; Pred. No. 1e-34;  
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNVLAWYQKPGKPKLLIYGASTLQSGVPS 60  
|||||  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNVLAWYQKPGKPKLLIYAASTLQSGVPS 60  
|||||  
QY 61 RPSGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106  
|||||  
Db 61 RPSGSGSGTDFLTITSSLPEDVATYYCQKFSPPPTFGPGTKVDI 106  
|||||

## RESULT 9

US-10-725-962-36  
; Sequence 36, Application US/10725962  
; Publication No. US20050013809A1  
; GENERAL INFORMATION:  
; APPLICANT: Samuel M. Owens  
; APPLICANT: Frank I. Carroll  
; APPLICANT: Philip Abraham  
; APPLICANT: Melinda G. Gunnell  
; APPLICANT: Mary Haak-Frendscho  
; APPLICANT: Xiao Feng  
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE  
; FILE REFERENCE: ABGENIX.071A  
; CURRENT APPLICATION NUMBER: US/10/725,962  
; CURRENT FILING DATE: 2003-12-02



```
US-10-041-860-32
Query Match          90.1%; Score 501; DB 14; Length 107;
Best Local Similarity 91.5%; Pred. No. 1.5e-34;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
QY 61 RFGSGSGTDFLTITISSLPEDVATYYCQKFSPPFTFGGTKVDI 106
DB 61 RFGSGSGTDFLTITISSLPEDVATYYCQKFSPPFTFGGTKVEI 106

RESULT 13
US-10-041-860-223
; Sequence 223, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX:051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-223

Query Match          90.1%; Score 501; DB 14; Length 107;
Best Local Similarity 91.5%; Pred. No. 1.5e-34;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
QY 61 RFGSGSGTDFLTITISSLPEDVATYYCQKFSPPFTFGGTKVDI 106
DB 61 RFGSGSGTDFLTITISSLPEDVATYYCQKFSPPFTFGGTKVEI 106

RESULT 14
US-10-041-860-257
; Sequence 257, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX:051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-257

Query Match          90.1%; Score 501; DB 14; Length 107;
Best Local Similarity 91.5%; Pred. No. 1.5e-34;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
QY 61 RFGSGSGTDFLTITISSLPEDVATYYCQKFSPPFTFGGTKVDI 106
DB 61 RFGSGSGTDFLTITISSLPEDVATYYCQKFSPPFTFGGTKVEI 106

RESULT 15
US-10-133-715-9
; Sequence 9, Application US/10133715
; Publication No. US20030206898A1
; GENERAL INFORMATION:
; APPLICANT: Fischkoff, Steven
; APPLICANT: Chartash, Elliot
; TITLE OF INVENTION: Use of TNF-a Antibodies and Another Drug
; FILE REFERENCE: BBI-186
; CURRENT APPLICATION NUMBER: US/10/133,715
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2SD4 light chain variable region
US-10-133-715-9

Query Match          90.1%; Score 501; DB 15; Length 107;
Best Local Similarity 89.6%; Pred. No. 1.5e-34;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIIRNYLAWYQONPGKVPKLLIYGASTLQSGVPS 60
QY 61 RFGSGSGTDFLTITISSLPEDVATYYCQKFSPPFTFGGTKVDI 106
DB 61 RFGSGSGTDFLTITISSLPEDVATYYCQKFSPPFTFGGTKVEI 106

Search completed: November 16, 2005, 23:05:44
Job time : 65.6949 secs
```

THE END OF THE LINE (1970)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 61.3676 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-34  
Perfect score: 556  
Sequence: 1 ELVMTQSPATLSVSPGERAT.....COQYNNWRTFGQTKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	107	7	Adc99805 Anti-huma
2	556	100.0	107	7	Ad005409 Anti-MUC1
3	556	100.0	107	7	Ad005442 Anti-MUC1
4	556	100.0	107	7	Adf09847 Human ant
5	546	98.2	107	7	Adc99777 Anti-huma
6	546	98.2	107	7	Ad005381 Anti-MUC1
7	546	98.2	107	7	Adf09819 Human ant
8	534	96.0	107	6	Abf54896 Light cha
9	530	95.3	107	6	Abf54900 Light cha
10	527	94.8	107	6	Abf54897 Light cha
11	527	94.8	107	6	Abf54883 Light cha
12	527	94.8	107	8	Adp22407 Human ant
13	527	94.8	107	8	Adp22404 Human ant
14	527	94.8	107	8	Adr31547 L16/JK4 h
15	527	94.8	107	6	Abf54891 Light cha
16	525	94.4	107	6	Abf54906 Light cha
17	524.5	94.3	108	6	Abf54893 Light cha
18	524	94.2	107	6	Abf54893 Light cha
19	524	94.2	107	8	Adp22408 Human ant
20	523	94.1	250	5	Abf45941 Human Bly
21	523	94.1	250	7	Adg96768 Single ch
22	521	93.7	107	6	Abf54889 Light cha
23	520.5	93.6	117	3	Aay99557 Human LHL
24	520.5	93.6	117	6	Abf42856 Tumour-sp
25	520.5	93.6	117	6	Abf42858 Tumour-sp

26	520.5	93.6	117	6	Abf42860 Tumour-sp
27	520.5	93.6	117	6	Abf42857 Tumour-sp
28	520.5	93.6	117	7	Abw02446 Human mon
29	520.5	93.6	117	7	Abw02466 Human mon
30	520.5	93.6	117	7	Abw02465 Human mon
31	520	93.5	246	5	Abp45257 Human Bly
32	520	93.5	246	7	Adg96084 Single ch
33	517	93.0	107	7	Adf080364 Human ant
34	516	92.8	107	8	Adp22278 Human ant
35	516	92.8	107	8	Adp22278 Human ant
36	516	92.8	127	7	Adc61110 Human ant
37	515.5	92.7	106	8	Adp22371 Human ant
38	515	92.6	154	8	Adl25472 Human mAb
39	513.5	92.4	117	6	Abf42850 Tumour-sp
40	513.5	92.4	117	6	Abf42851 Tumour-sp
41	513.5	92.4	117	6	Abf42849 Tumour-sp
42	513.5	92.4	117	6	Abf42853 Tumour-sp
43	513.5	92.4	117	7	Abw02460 Human mon
44	513.5	92.4	117	7	Abw02462 Human mon
45	513.5	92.4	117	7	Abw02459 Human mon

ALIGNMENTS

RESULT 1  
ADC99805  
ID ADC99805 standard; protein; 107 AA.  
XX  
AC ADC99805;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 34.  
XX  
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
KW lung cancer; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057838-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041581.  
XX  
PR 28-DEC-2001; 2001US-0346299P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas J;  
XX  
XX WPI; 2003-587113/55.  
DR N-PSDB; ADC99807.  
XX  
PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
PT or condition associated with expression of MUC18 in a patient, e.g.  
PT tumors, cancers, and other malignancies.  
XX  
PS Claim 3; SEQ ID NO 34; 78pp; English.  
XX  
CC The invention relates to a novel isolated monoclonal antibody comprising  
CC a heavy or light chain amino acid or a heavy or light chain variable  
CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
CC invention demonstrates cytostatic activity and may be useful for treating  
CC a disease or condition associated with the expression of MUC18 on the  
CC cell surface such as tumours, specifically melanoma, oesophageal,  
CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
CC carcinomas and cervical intraepithelial neoplasia and cancers including  
CC colorectal, breast or lung cancer, as well as other malignancies. The  
CC current sequence is that of the anti-human MUC18 monoclonal antibody

CC light chain protein of the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 556; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 3.1e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNWPRFTFGQTKVEIK 107

Db 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNWPRFTFGQTKVEIK 107

RESULT 2

ADD05409

ID ADD05409 standard; protein; 107 AA.

XX

AC ADD05409;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 34.

XX

KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

XX

KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.

XX

OS Homo sapiens.

XX

PN WO2003057006-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041582.

XX

PR 28-DEC-2001; 2001US-0346460P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Bar-Eli M;

XX

DR WPI; 2003-577496/54.

XX

DR N-PSDB; ADD05411.

XX

PS Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

PT treating tumors, inhibiting tumor growth, inhibiting cell invasion

PT associated with melanoma, or increasing survival of an animal having a

PT metastatic tumor.

XX

PS Claim 3; SEQ ID NO 34; 87pp; English.

XX

CC The invention relates to a novel monoclonal antibody used for inhibiting

CC tumour growth in an animal. The tumour inhibition process comprises

CC selecting an animal in need of treatment for a tumour, providing a

CC monoclonal antibody comprising a heavy chain amino acid, where the

CC antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody

CC binds MUC18, and contacting the tumour with the antibody resulting in

CC inhibited proliferation of the cells. The monoclonal antibody has

CC cytostatic and can be used in the production of a vaccine. The monoclonal

CC antibodies against the MUC18 antigen are useful for diagnosing and

CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

CC tumour metastasis), inhibiting cell invasion associated with melanoma, or

CC increasing survival of an animal having a metastatic tumour. This

CC sequence represents an anti-MUC18 antibody light chain, variable region,

CC protein of the invention.

XX

SQ Sequence 107 AA;

XX

Query Match 100.0%; Score 556; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 3.1e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNWPRFTFGQTKVEIK 107

Db 61 RPSGSGSGTEFTLTISLSQSEDFAVYCCQYNWPRFTFGQTKVEIK 107

RESULT 3

ADD05442

ID ADD05442 standard; protein; 107 AA.

XX

AC ADD05442;

XX

DT 01-JAN-2004 (first entry)

XX

DE Anti-MUC18 antibody light chain variable region L2 protein, SEQ ID 67.

XX

KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;

XX

KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.

XX

OS Unidentified.

XX

PN WO2003057006-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041582.

XX

PR 28-DEC-2001; 2001US-0346460P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Bar-Eli M;

XX

DR WPI; 2003-577496/54.

XX

PS Use of monoclonal antibodies against MUC18 antigen, for diagnosing and

PT treating tumors, inhibiting tumor growth, inhibiting cell invasion

PT associated with melanoma, or increasing survival of an animal having a

PT metastatic tumor.

XX

PS Disclosure; SEQ ID NO 67; 87pp; English.

XX

CC The invention relates to a novel monoclonal antibody used for inhibiting

CC tumour growth in an animal. The tumour inhibition process comprises

CC selecting an animal in need of treatment for a tumour, providing a

CC monoclonal antibody comprising a heavy chain amino acid, where the

CC antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody

CC binds MUC18, and contacting the tumour with the antibody resulting in

CC inhibited proliferation of the cells. The monoclonal antibody has

CC cytostatic and can be used in the production of a vaccine. The monoclonal

CC antibodies against the MUC18 antigen are useful for diagnosing and

CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or

CC tumour metastasis), inhibiting cell invasion associated with melanoma, or

CC increasing survival of an animal having a metastatic tumour. This

CC sequence represents an anti-MUC18 antibody light chain, variable region,

CC protein of the invention.

XX

SQ Sequence 107 AA;

XX

Query Match 100.0%; Score 556; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 3.1e-34;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLIFGASTRAITGIPA 60

QY 61 RFGSGSGTEFTLTISLQSEDFAVYVCOQYNNWPRFTFGGKVEIK 107  
 DB 61 RFGSGSGTEFTLTISLQSEDFAVYVCOQYNNWPRFTFGGKVEIK 107

RESULT 4  
 ADF09847  
 ID ADF09847 standard; protein; 107 AA.  
 AC ADF09847;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody light chain #9.  
 KW cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; light chain; human.  
 XX  
 OS Homo sapiens.  
 PN WO2003057837-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041580.  
 XX  
 PR 28-DEC-2001; 2001US-0346414P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-598367/56.  
 DR N-PSDB; ADF09849.  
 XX  
 PT Inhibiting cell proliferation associated with expression of MUC18 tumour  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.  
 XX  
 PS Claim 3; SEQ ID NO 34; 83pp; English.  
 XX  
 CC The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a light chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 100.0%; Score 556; DB 7; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-34;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFANFYQKPGQAPRLIFGASTRATGIPA 60  
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFANFYQKPGQAPRLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLQSEDFAVYVCOQYNNWPRFTFGGKVEIK 107  
 DB 61 RFGSGSGTEFTLTISLQSEDFAVYVCOQYNNWPRFTFGGKVEIK 107

RESULT 5  
 ADC99777  
 ID ADC99777 standard; protein; 107 AA.  
 XX

AC ADC99777;  
 XX  
 DT 01-JAN-2004 (first entry)  
 DE  
 DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 6.  
 XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057838-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041581.  
 XX  
 PR 28-DEC-2001; 2001US-0346299P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-587113/55.  
 DR N-PSDB; ADC9779.  
 XX  
 PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 XX  
 PS Claim 3; SEQ ID NO 6; 78pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC light chain protein of the invention.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 98.2%; Score 546; DB 7; Length 107;  
 Best Local Similarity 97.2%; Pred. No. 1.7e-33;  
 Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFANFYQKPGQAPRLIFGASTRATGIPA 60  
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFANFYQKPGQAPRLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLQSEDFAVYVCOQYNNWPRFTFGGKVEIK 107  
 DB 61 RFGSGSGTEFTLTISLQSEDFAVYVCOQYNNWPRFTFGGKVEIK 107

RESULT 6  
 ADD05381  
 ID ADD05381 standard; protein; 107 AA.  
 XX  
 AC ADD05381;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-MUC18 antibody light chain variable region protein, SEQ ID No 6.  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.





```
XX DR WPI; 2003-313359/30.
XX PT Amplifying nucleic acid by contacting engineered nucleic acid strand
XX PT having predetermined sequence at one end and sequence complementary to
XX PT predetermined sequence at other end, with primer having predetermined
XX PS sequence.
XX PS Example 3; Fig 8b-c; 68pp; English.
XX CC The present invention describes a method (M1) for amplifying a nucleic
XX CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other, and contacting (S) with a
XX CC primer having the predetermined sequence in the presence of a polymers
XX CC and nucleotides under conditions suitable for polymerisation of the
XX CC nucleotides. Also described is an engineered nucleic acid strand (I)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other end. M1 is useful for
XX CC amplifying a nucleic acid. M1 can be used for producing an antibody
XX CC library. M1 is useful for preparing amplified products that can be
XX CC ligated into a suitable expression vector, where the vector can be used
XX CC to transform an appropriate host organism to produce the polypeptide or
XX CC protein encoded by the target sequence. M1 is useful to amplify a family
XX CC of related sequences to build a complex library such as, for example an
XX CC antibody library. M1 is useful not only for producing large amounts of
XX CC one target nucleic acid sequence, but also for amplifying simultaneously
XX CC more than one different target nucleic acid sequence located on the same
XX CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
XX CC ABR54998 represent sequence used in the exemplification of the present
XX CC invention
XX SQ Sequence 107.AA;

Query Match 96.0%; Score 534; DB 6; Length 107;
Best Local Similarity 95.3%; Pred. No. 1.4e-32; Indels 0; Gaps 0;
Matches 102; Conservative 3; Mismatches 2;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFAWYQQKPGQAPRLLIIFGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTITSSIQSEDFAVYYCQYNNWPRFTGGTKVEIK 107
DB 61 RFGSGSGTFTLTITSSIQSEDFAVYYCQYNNWPRFTGGTKVEIK 107

RESULT 9
ABR54900
ID ABR54900 standard; protein; 107 AA.
XX AC ABR54900;
XX DT 30-JUN-2003 (first entry)
XX DE Light chain clone HBPAXK2d 3D12 SEQ ID NO:126.
XX KW Engineered template; single primer amplification; antibody library;
XX KW nucleic acid amplification.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003025202-A2.
XX PD 27-MAR-2003.
XX PF 19-SEP-2002; 2002WO-US029889.
XX PR 19-SEP-2001; 2001US-0323455P.
XX PA (ALEX-) ALEXION PHARM INC.
XX
```

```
PI Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
XX WPI; 2003-313359/30.
XX PT Amplifying nucleic acid by contacting engineered nucleic acid strand
XX PT having predetermined sequence at one end and sequence complementary to
XX PT predetermined sequence at other end, with primer having predetermined
XX PS sequence.
XX PS Example 3; Fig 8b-c; 68pp; English.
XX CC The present invention describes a method (M1) for amplifying a nucleic
XX CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other, and contacting (S) with a
XX CC primer having the predetermined sequence in the presence of a polymers
XX CC and nucleotides under conditions suitable for polymerisation of the
XX CC nucleotides. Also described is an engineered nucleic acid strand (I)
XX CC having a predetermined sequence at one end and a sequence complementary
XX CC to the predetermined sequence at the other end. M1 is useful for
XX CC amplifying a nucleic acid. M1 can be used for producing an antibody
XX CC library. M1 is useful for preparing amplified products that can be
XX CC ligated into a suitable expression vector, where the vector can be used
XX CC to transform an appropriate host organism to produce the polypeptide or
XX CC protein encoded by the target sequence. M1 is useful to amplify a family
XX CC of related sequences to build a complex library such as, for example an
XX CC antibody library. M1 is useful not only for producing large amounts of
XX CC one target nucleic acid sequence, but also for amplifying simultaneously
XX CC more than one different target nucleic acid sequence located on the same
XX CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
XX CC ABR54998 represent sequence used in the exemplification of the present
XX CC invention
XX SQ Sequence 107.AA;

Query Match 95.3%; Score 530; DB 6; Length 107;
Best Local Similarity 94.4%; Pred. No. 2.7e-32; Indels 0; Gaps 0;
Matches 101; Conservative 3; Mismatches 3;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFAWYQQKPGQAPRLLIIFGASTRATGIPA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTFTLTITSSIQSEDFAVYYCQYNNWPRFTGGTKVEIK 107
DB 61 RFGSGSGTFTLTITSSIQSEDFAVYYCQYNNWPRFTGGTKVEIK 107

RESULT 10
ABR54897
ID ABR54897 standard; protein; 107 AA.
XX AC ABR54897;
XX DT 30-JUN-2003 (first entry)
XX DE Light chain clone HBPAXK2d 3A12 SEQ ID NO:123.
XX KW Engineered template; single primer amplification; antibody library;
XX KW nucleic acid amplification.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003025202-A2.
XX PD 27-MAR-2003.
XX PF 19-SEP-2002; 2002WO-US029889.
XX PR 19-SEP-2001; 2001US-0323455P.
XX PA (ALEX-) ALEXION PHARM INC.
XX
```



OS Homo sapiens.  
 PN WO2004050683-A2.  
 PD 17-JUN-2004.  
 PP 02-DEC-2003; 2003WO-US038281.  
 PR 02-DEC-2002; 2002US-0430729P.  
 XX (ABGE-) ABGENIX INC.  
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX WPI; 2004-480601/45.  
 XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX Example 10; SEQ ID NO 310; 213pp; English.  
 PS The present invention describes a human monoclonal antibody (I) that  
 XX specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFa in a patient sample, comprising contacting with  
 CC the sample; (2) a composition comprising the antibody and TNFa in  
 CC the sample; and (3) treating (M2) an animal suffering from a  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFa induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiartherosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoisiatric, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFa  
 CC antibody light chain variable region, which is used in the  
 XX exemplification of the present invention.  
 XX Sequence 107 AA;  
 SQ  
 Query Match 94.8%; Score 527; DB 8; Length 107;  
 Best Local Similarity 93.5%; Pred. No. 4.5e-32;  
 Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNPAWYQKPGQAPRLIFGASTRATGIPA 60  
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSSNNLAWYQKPGQAPRLIFGASTRATGIPA 60  
 QY 61 RFSGSGSGTEFTLTISLSQSEDPFVYCCQYNNWPRFTGGQKVEIK 107  
 DB 61 RFSGSGSGTEFTLTISLSQSEDPFVYCCQYNNWPRFTGGQKVEIK 107

RESULT 13  
 ADP22407

ID ADP22407 standard; protein; 107 AA.  
 AC ADP22407;  
 XX 09-SEP-2004 (first entry)  
 DT Human anti-TNFA antibody light chain variable region SEQ ID NO:313.  
 DE human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
 KW anti-TNFA antibody; anabolic; antiartherosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoisiatric; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.  
 XX Homo sapiens.  
 OS WO2004050683-A2.  
 PN 17-JUN-2004.  
 PD 02-DEC-2003; 2003WO-US038281.  
 XX 02-DEC-2002; 2002US-0430729P.  
 PR (ABGE-) ABGENIX INC.  
 PA Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX WPI; 2004-480601/45.  
 XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX Example 10; SEQ ID NO 313; 213pp; English.  
 PS The present invention describes a human monoclonal antibody (I) that  
 XX specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFa in a patient sample, comprising contacting with  
 CC the sample; (2) a composition comprising the antibody and TNFa in  
 CC the sample; and (3) treating (M2) an animal suffering from a  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFa induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiartherosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoisiatric, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody light chain variable region, which is used in the  
 XX exemplification of the present invention.

CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody light chain variable region, which is used in the  
 CC exemplification of the present invention.

XX  
 SQ Sequence 107 AA;

Query Match 94.8%; Score 527; DB 8; Length 107;  
 Best Local Similarity 94.4%; Pred. No. 4.5e-32;  
 Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNFAWYQQKPGAPRLIFGASTRATGIPA 60  
 DB 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNFAWYQQKPGAPRLIFGASTRATGIPA 60  
 QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
 DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 14  
 ADR43402  
 ID ADR43402 standard; protein; 107 AA.  
 XX  
 AC ADR43402;  
 DT 04-NOV-2004 (first entry)  
 XX Human anti-IgE antibody light chain L16 and JK4.  
 DE  
 KW antibody; variable light chain; variable heavy chain; Antiallergic;  
 KW Dermatological; Immunosuppressive; IGE; asthma; allergic rhinitis;  
 KW eczema; urticaria; atopic dermatitis; food allergy; CDR.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004070011-A2.  
 PD 19-AUG-2004.  
 XX  
 PF 02-FEB-2004; 2004WO-US002894.  
 XX  
 PR 01-FEB-2003; 2003US-0444229P.  
 XX (TANO-) TANOX INC.  
 XX Singh S, Foster C, Wu H;  
 XX WPI; 2004-604433/58.  
 XX  
 PT New high affinity human monoclonal antibodies, particularly those  
 PT directed against isotopic determinants of immunoglobulin E, useful for  
 PT asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a  
 PT food allergy.  
 XX  
 PS Disclosure; SEQ ID NO 2; 101pp; English.  
 XX  
 CC The present invention relates to an antibody comprising a variable light  
 CC chain region or a variable heavy chain region. The antibody and methods  
 CC are useful for treating a disorder associated with an abnormally high IGE  
 CC level, e.g. asthma, allergic rhinitis, eczema, urticaria, atopic  
 CC dermatitis, or a food allergy. The present sequence represents human anti  
 CC -IGE antibody light chain combined L16 and JK4.  
 XX  
 SQ Sequence 107 AA;

Query Match 94.8%; Score 527; DB 8; Length 107;  
 Best Local Similarity 94.4%; Pred. No. 4.5e-32;  
 Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNFAWYQQKPGAPRLIFGASTRATGIPA 60  
 DB 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNFAWYQQKPGAPRLIFGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
 DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 15  
 ADR31547  
 ID ADR31547 standard; protein; 107 AA.  
 XX  
 AC ADR31547;  
 DT 04-NOV-2004 (first entry)  
 XX L16/JK4 human light chain consensus sequence template.  
 DE  
 KW Antibody; diagnostic; prophylaxis; therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 24..34 /note= "Kabat CDR"  
 FT Region 50..56 /note= "Kabat CDR"  
 FT Region 89..97 /note= "Kabat CDR"  
 FT  
 XX WO2004070010-A2.  
 PN  
 PD 19-AUG-2004.  
 XX  
 PF 02-FEB-2004; 2004WO-US002892.  
 XX  
 PR 01-FEB-2003; 2003US-0444229P.  
 XX (TANO-) TANOX INC.  
 XX Singh S, Foster C, Wu H;  
 XX WPI; 2004-604432/58.  
 DR  
 XX  
 PT Generating a humanized, high affinity antibody from an antibody of  
 PT interest comprises selecting a suitable human template as the framework  
 PT for the H and L chain variable domains of the high affinity antibody to  
 PT be made.  
 XX  
 PS Example 1; SEQ ID NO 2; 100pp; English.  
 XX  
 CC The invention relates to a method for generating a humanised high  
 CC affinity antibody from an antibody of interest. The method involves  
 CC selecting a suitable human template as the framework for the H (heavy)  
 CC and L (light) chain variable (V) domains of the high affinity antibody to  
 CC be made. The method is useful for generating high affinity antibodies  
 CC useful in diagnostics, prophylaxis and treatment of diseases. The present  
 CC sequence is L16/JK4 human light chain consensus sequence template. This  
 CC sequence is used in the exemplification of the invention.  
 XX  
 SQ Sequence 107 AA;

Query Match 94.8%; Score 527; DB 8; Length 107;  
 Best Local Similarity 94.4%; Pred. No. 4.5e-32;  
 Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNFAWYQQKPGAPRLIFGASTRATGIPA 60  
 DB 1 EIVMTQSPATLSVSPGERATLSCRSQSISNNFAWYQQKPGAPRLIFGASTRATGIPA 60  
 QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107  
 DB 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

Search completed: November 16, 2005, 21:51:43

Job time : 62.3676 secs

---

END PAGE BLANK (USPTO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-34  
Perfect score: 556  
Sequence: 1 EIVMTQSPATLSVSPGERAT.....COQYNWPRTFGGTKVEIK 107  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	535	96.2	107	2	S34005	Ig kappa chain V r
2	527	94.8	117	2	S40362	Ig kappa chain - h
3	522	93.9	128	2	S40343	Ig kappa chain V-J
4	504.5	90.7	109	1	K3HUPM	Ig kappa chain V-I
5	490.5	88.2	131	2	S40328	Ig kappa chain - h
6	486.5	87.5	116	2	B26555	Ig kappa chain V-I
7	486	87.4	128	2	A56701	Ig kappa chain V r
8	482	86.7	111	2	S23628	Ig kappa chain V r
9	481.5	86.6	215	2	JE0244	Ig kappa chain NIG
10	475	85.4	115	1	K3HUCI	Ig kappa chain pre
11	474	85.3	115	2	A30553	Ig kappa chain pre
12	474	85.3	215	2	JE0243	Ig kappa chain NIG
13	473	85.1	144	2	PL0106	Ig kappa chain pre
14	467.5	84.1	109	2	K30601	Ig kappa chain V-I
15	466.5	83.9	129	1	K3H0HA	Ig kappa chain pre
16	464.5	83.5	109	2	F30607	Ig kappa chain V-I
17	464	83.5	98	2	PH0868	Ig kappa chain V r
18	464	83.5	98	2	I30608	Ig kappa chain V-I
19	463.5	83.4	114	2	S54905	Ig kappa chain V r
20	462	83.1	110	2	S40326	Ig kappa chain V-J
21	462	83.1	123	2	S40378	Ig kappa chain - h
22	462	83.1	128	2	S40379	Ig kappa chain V-I
23	461.5	83.0	109	1	K3HUSI	Ig kappa chain V-I
24	460.5	82.8	109	2	K30601	Ig kappa chain V-I
25	460.5	82.8	128	2	S20636	Ig kappa chain V r
26	460.5	82.8	129	2	A32274	Ig kappa chain pre
27	459.5	82.6	109	2	G30601	Ig kappa chain V-I
28	459	82.6	91	2	S37527	Ig kappa chain V r
29	459	82.6	108	2	G44151	Ig kappa chain V r

RESULT 1  
S34005  
Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S34005; S30524  
R:Mariette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A>Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A:Reference number: S34001; MUID:93209281; PMID:7681398  
A:Accession: S34005  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-107 <MAP>  
A:Cross-references: EMBL:X18330  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

ALIGNMENTS

RESULT 1

Query Match 96.2%; Score 535; DB 2; Length 107;  
Best Local Similarity 95.3%; Pred. No. 3.3e-39;  
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNFAYVQKPGQAPRLLIIGASTRATGIPA 60  
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIIGASTRATGIPA 60  
QY 61 RPSGSGSGTEFTLTISLSQSEDFAVYVCOQYNWPRTFGGTKVEIK 107  
Db 61 RPSGSGSGTEFTLTISLSQSEDFAVYVCOQYNWPRTFGGTKVEIK 107

RESULT 2

S40362  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40362  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40362  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-117 <KLE>  
A:Cross-references: EMBL:X72472; NID:G441412; PID:G441413  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 527; DB 2; Length 117;

```
Best Local Similarity 94.4%; Pred. No. 1.7e-38; Mismatches 3; Indels 0; Gaps 0;
Matches 101; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIIFGASTRATGIPA 60
Db 11 EIVMTQSPATLSVSPGERATLSCRASQSISSNLAWYQKPGQAPRLLIIFGASTRATGIPA 70
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 71 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 117

RESULT 3
S40343
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40343
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40343
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: EMBL:X72453; NID:g441374; PIDN:CAAS1121.1; PID:g441375
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 522; DB 2; Length 128;
Best Local Similarity 92.3%; Pred. No. 5.1e-38; Mismatches 3; Indels 0; Gaps 0;
Matches 99; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIIFGASTRATGIPA 60
Db 21 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIIFGASTRATGIPA 80
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 81 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKLEIK 127

RESULT 4
K3HUPM
Ig kappa chain V-III region (Pom) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01897
R:Klapper, D.G.; Capra, J.D.
Ann. Immunol. (Inst. Pasteur) 127C, 261-271, 1976
A:Title: The amino acid sequence of the variable regions of the light chains from two id
A:Reference number: A01897
A:Accession: A01897
A:Molecule type: protein
A:Residues: 1-109 <KLA>
C:Cross-references: UNIPROT:P01624
C:Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:15-91/Domain: immunoglobulin homology <IMM>
F:23-89/Disulfide bonds: #status predicted

Query Match 90.7%; Score 504.5; DB 1; Length 109;
Best Local Similarity 90.7%; Pred. No. 1.4e-36; Mismatches 4; Indels 1; Gaps 1;
Matches 98; Conservative
```

```
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIIFGASTRATGIP 59
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNLAWYQKPGQAPRLLIIFGASTRATGIP 60
QY 60 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKRVEIK 108

RESULT 5
S40328
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40328
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40328
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72438; NID:g441344; PIDN:CAAS1106.1; PID:g441345
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-109/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 490.5; DB 2; Length 131;
Best Local Similarity 87.0%; Pred. No. 2.6e-35; Mismatches 6; Mismatches 7; Indels 1; Gaps 1;
Matches 94; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIIFGASTRATGIPA 60
Db 20 EIVMTQSPATLSVSPGERATLSCRASQSVIHNLAWYQKPGQAPRLLIIFGAYTRATGVPA 79
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 80 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 127

RESULT 6
B26555
Ig kappa chain V-III region (Ger) - human
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26555
R:Midhaugh, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A:Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
A:Reference number: A92630; MUID:87137666; PMID:3102493
A:Accession: B26555
A:Molecule type: protein
A:Residues: 1-116 <MID>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 486.5; DB 2; Length 116;
Best Local Similarity 88.0%; Pred. No. 5.1e-35; Mismatches 7; Mismatches 5; Indels 1; Gaps 1;
Matches 95; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIIFGASTRATGIPA 60
Db 1 DIYMTQVPATLSVSPGERATLSCRASQSISSNLAWYQKPGQAPRLLIIFGASTRATGIPA 60
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKRLEIK 108

RESULT 7
B26555
Ig kappa chain V-III region (Ger) - human
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26555
R:Midhaugh, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A:Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
A:Reference number: A92630; MUID:87137666; PMID:3102493
A:Accession: B26555
A:Molecule type: protein
A:Residues: 1-116 <MID>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 486.5; DB 2; Length 116;
Best Local Similarity 88.0%; Pred. No. 5.1e-35; Mismatches 7; Mismatches 5; Indels 1; Gaps 1;
Matches 95; Conservative

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSISSNNFVWYQKPGQAPRLLIIFGASTRATGIPA 60
Db 1 DIYMTQVPATLSVSPGERATLSCRASQSISSNLAWYQKPGQAPRLLIIFGASTRATGIPA 60
QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKRLEIK 108

RESULT 7
```







C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>  
F;21-117/Region: V segment  
F;36-111/Domain: immunoglobulin homology <IMM>  
F;44-55/Region: complementarity-determining 1  
F;71-77/Region: complementarity-determining 2  
F;110-117/Region: complementarity-determining 3  
F;118-129/Region: J segment (JK1)  
F;43-109/Disulfide bonds: #status predicted

Query Match	83.9%;	Score 466.5;	DB 1;	Length 129;
Best Local Similarity	83.3%;	Pred. No. 2.9e-33;		
Matches	90;	Conservative 10;	Mismatches 7;	Indels 1; Gaps 1;

QY	1	EIVMTQSPATLSVSPGERATLSCRASQSIENNIF-AWYQKPGQAPRLLI FGASTRATGIP	59
Db	21	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIP	80

QY	60	ARFSGSGSGTEFTLTITISQLQSEDFAVYCCQYNWNPRTFGQGTKVEIK	107
Db	81	DRFSGSGSGTDFLTITISRLPEDFAVYCCQYGTSPRTFGQGTKVEIK	128

Search completed: November 16, 2005, 22:04:10  
Job time : 13.7849 secs

THE NEEDS (1979)

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-34

Perfect score: 556

Sequence: 1 BIVMTQSPATLSVSPGERAT.....CQQYNWPRTPGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	515.5	92.7	129	1	KV3H_HUMAN	P04207 homo sapien
2	504.5	90.7	109	1	KV3F_HUMAN	P01624 homo sapien
3	504	90.6	108	2	Q9UL83	Q9ul83 homo sapien
4	498.5	89.7	109	2	Q9UL85	Q9ul85 homo sapien
5	488.5	87.9	235	2	O6GMW0	O6gmw0 homo sapien
6	466.5	83.9	129	1	KV3L_HUMAN	P18135 homo sapien
7	461.5	83.0	109	1	KV3B_HUMAN	P01620 homo sapien
8	458.5	82.5	109	1	KV3D_HUMAN	P01622 homo sapien
9	454.5	81.7	109	1	KV3E_HUMAN	P01623 homo sapien
10	453.5	81.6	129	1	KV3M_HUMAN	P18136 homo sapien
11	445.5	80.1	109	2	Q9UL78	Q9ul78 homo sapien
12	437.5	78.7	109	1	KV3G_HUMAN	P04206 homo sapien
13	435.5	78.3	108	1	KV3A_HUMAN	P01619 homo sapien
14	435.5	78.3	235	2	O6PJF2	O6pjf2 homo sapien
15	430.5	77.4	235	2	O6GMV9	O6gmw9 homo sapien
16	429	77.2	115	1	KV31_HUMAN	P04433 homo sapien
17	428	77.0	128	1	KV3K_HUMAN	P06311 homo sapien
18	428	77.0	236	2	O6PIL8	O6pil8 homo sapien
19	423	76.1	108	1	KVIM_HUMAN	P01605 homo sapien
20	422.5	76.0	109	2	Q9UL86	Q9ul86 homo sapien
21	422	75.9	236	2	O6P5S8	O6p5s8 homo sapien
22	415	74.6	108	2	Q9UL79	Q9ul79 homo sapien
23	411	73.9	134	1	KVAC_HUMAN	O66314 homo sapien
24	409.5	73.7	116	1	KV3J_HUMAN	P04434 homo sapien
25	400	71.9	108	2	Q9UL70	Q9ul70 homo sapien
26	400	71.9	236	2	O6GMW1	O6gmw1 homo sapien
27	399	71.8	114	1	KV4A_HUMAN	P01625 homo sapien
28	398.5	71.7	100	1	KV3C_HUMAN	P01621 homo sapien
29	398	71.6	108	1	KVIR_HUMAN	P01610 homo sapien
30	398	71.6	236	2	O6PIH7	O6pih7 homo sapien
31	398	71.6	236	2	O6PII5	O6pii5 homo sapien

Query Match

92.7% ; Score 515.5; DB 1; Length 129;

32	396	71.2	234	2	Q7Z473	Q7z473 homo sapien
33	395	71.0	108	1	KVIG_HUMAN	P01599 homo sapien
34	393.5	70.8	133	1	KV4B_HUMAN	P06313 homo sapien
35	393	70.7	108	1	KV1F_HUMAN	P01598 homo sapien
36	393	70.7	108	1	KV1V_HUMAN	P04430 homo sapien
37	393	70.7	236	2	Q7Z3Y4	Q7z3y4 homo sapien
38	393	70.7	244	2	O65ZC8	O65zc8 homo sapien
39	390	70.1	108	1	KVIL_HUMAN	P01604 homo sapien
40	389	70.0	236	2	O6GMX8	O6gmx8 homo sapien
41	388	69.8	240	2	O65ZC9	O65zc9 homo sapien
42	387	69.6	255	2	O6KB05	O6kb05 mus musculu
43	386	69.4	108	1	KV1Q_HUMAN	P01609 homo sapien
44	386	69.4	108	1	KV1Y_HUMAN	P80362 homo sapien
45	385	69.2	108	1	KV1H_HUMAN	P01600 homo sapien

#### ALIGNMENTS

RESULT 1  
KV3H\_HUMAN  
ID KV3H\_HUMAN STANDARD; PRT; 129 AA.  
AC P04207;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86177570; PubMed=3083417;  
RA Jirik P.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,  
RA Goldfien R., Carson D.A.;  
RT "Cloning and sequence determination of a human rheumatoid factor  
light-chain gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
EMBL; M12740; AA58992.1; -  
HSSP; P01625; ILVE.  
GO; GO:0005576; C:extracellular; NAS.  
GO; GO:0003823; F:antigen binding; NAS.  
GO; GO:0006955; P:immune response; NAS.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003596; IG\_v.  
Pfam; PF00047; Ig; 1.  
SMART; SMO0406; IGV; 1.  
PROSITE; PS50835; IG\_LIKE; 1.  
Immunoglobulin V region; Signal.  
SIGNAL 1 20  
CHAIN 21 129 Ig kappa chain V-III region CLL.  
FT DOMAIN 21 43 Framework-1.  
FT DOMAIN 44 54 Complementarity-determining-1.  
FT DOMAIN 55 69 Framework-2.  
FT DOMAIN 70 76 Complementarity-determining-2.  
FT DOMAIN 77 108 Framework-3.  
FT DOMAIN 109 118 Complementarity-determining-3.  
FT DOMAIN 119 129 Jk1 segment.  
FT DISULFID 43 108 By similarity.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BB60CC14 CRC64;

```
Best Local Similarity 92.6%; Pred. No. 6.1e-48;
Matches 100; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIIFGASTRATGIPA 60
DB 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 80
QY 61 RFGSGSGTFTLTITSSLSQSEDFAVYCCQYNNWPR-TFGQGTKEIK 107
DB 81 RFGSGSGTFTLTITSSLSQSEDFAVYCCQYNNWPPFTFGQGTKEIK 128

RESULT 2
ID KV3F HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IgM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
CC PIR; A01897; K3HUPM.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DPC6A8ABA86 CRC64;

Query Match 90.7%; Score 504.5; DB 1; Length 109;
Best Local Similarity 90.7%; Pred. No. 7.9e-47;
Matches 98; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIIFGASTRATGIP 59
DB 1 EIVMTQSPVTLSPGERATLSCRASQSIINSYLAWYQKPSGPRLLIYGASTRATGIP 60
QY 60 ARFSGSGTFTLTITSSLSQSEDFAVYCCQYNNWPR-TFGQGTKEIK 107
DB 61 ARFSGSGTFTLTITSSLSQSEDFAVYCCQYNNWPPFTFGQGTKEIK 108

RESULT 3
QYUL83 PRELIMINARY; PRT; 108 AA.
AC QYUL83;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Best Local Similarity 89.7%; Score 498.5; DB 2; Length 109;
Matches 98; Conservative 5; Mismatches 4; Indels 1; Gaps 1;
```

```
QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISSNNFAVYQOQPGQAPRLLIIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRSQSISSNNFAVYQOQPGQAPRLLIIFGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFQGQTKVEIK 107
Db 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFQGQTKVEIK 108

RESULT 5
Q6GMW0 PRELIMINARY; PRT; 235 AA.
AC O6GMW0;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG_LIKE; 2.
DR PROSITE; PS00230; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;
```

```
Query Match 87.9%; Score 488.5; DB 2; Length 235;
Best Local Similarity 88.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISSNNFAVYQOQPGQAPRLLIIFGASTRATGIPA 60
Db 21 EIVMTQSPATLSVSPGERATLSCRSQSISSNNFAVYQOQPGQAPRLLIIFGASTRATGIP 80
```

```
QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFQGQTKVEIK 107
Db 81 RFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFQGQTKVEIK 128

RESULT 6
KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RT J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
leukemia.
CC autoantibodies expressed in patients with chronic lymphocytic
leukemia.
DR PIR; P10022; K3HUHA.
DR HSSP; P01625; 1EEQ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 55 Complementarity-determining-1.
FT DOMAIN 56 70 Framework-2.
FT DOMAIN 71 77 Complementarity-determining-2.
FT DOMAIN 78 109 Framework-3.
FT DOMAIN 110 118 Complementarity-determining-3.
FT DOMAIN 119 129 JkI segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;
```

```
Query Match 83.9%; Score 466.5; DB 1; Length 129;
Best Local Similarity 83.3%; Pred. No. 1.3e-42;
Matches 90; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRSQSISSNNFAVYQOQPGQAPRLLIIFGASTRATGIP 59
Db 21 EIVLTQSPCTLSLSPGERATLSCRSQSVSSSYLAWYQOQPGAPRLLIYGASSTRATGIP 80

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYCCQYNNW-PRTFQGQTKVEIK 107
Db 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYNGTSPRTFGQGTKEIK 128
```

```
RESULT 7
KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
```

```

DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01892; K3HUSI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 83.0%; Score 461.5; DB 1; Length 109;
Best Local Similarity 81.5%; Pred. No. 3 6e-42;
Matches 88; Conservative 13; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNF-AMYQKPKGQAPRLLIIFGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVNSFLAWYQKPKGQAPRLLIYGASSRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107
Db 61 DRFSGSGSGTDFLTISRLEPEDFAVYYCOQYSGSPSTFGQGTKEIK 108

RESULT 8
KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for the
RT mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUTI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

```

```

DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 82.5%; Score 458.5; DB 1; Length 109;
Best Local Similarity 82.4%; Pred. No. 7.7e-42;
Matches 89; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNF-AMYQKPKGQAPRLLIIFGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVNSFLAWYQKPKGQAPRLLIYVASSRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107
Db 61 DRFSGSGSGTDFLTISRLEPEDFAVYYCOQYSGSPSTFGQGTKEIK 108

RESULT 9
KV3E_HUMAN STANDARD; PRT; 109 AA.
ID KV3E_HUMAN
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01896; K3HJML.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 81.7%; Score 454.5; DB 1; Length 109;
Best Local Similarity 81.5%; Pred. No. 2.1e-41;
Matches 88; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNF-AMYQKPKGQAPRLLIIFGASTRATGIP 59
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVNSFLAWYQKPKGQAPRLLIYVASSRATGIP 60

QY 60 ARFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNWPRTFGQGTKEIK 107
Db 61 DRFSGSGSGTDFLTISRLEPEDFAVYYCOQYSGSLGRTFGQGTKEIK 108

RESULT 10

```







ID O6GMV9 PRELIMINARY; PRT; 235 AA.  
AC O6GMV9;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073793; AAH73793.1; --  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein\_  
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 77.4%; Score 430.5; DB 2; Length 235;  
Best Local Similarity 76.9%; Pred. No. 2.1e-38;  
Matches 83; Conservative 12; Mismatches 12; Indels 1; Gaps 1;  
QY 1 EIVMTQSPATLSVSPGERATLSCRASQISNNP-ANYQOKPGQAPRLILFGASTRATGIP 59  
DB 21 EIVLTQSPGTLSPGERAALSCRASQVNSKYLAWYQOKPGQAPRLMLYAAASIRATGIP 80  
QY 60 ARFSGSGSGTEFTLTSSLSQSEDFAVYVCOQYNNWPRTFGQGTKVEIK 107  
DB 81 DRFSGSGSGTEFTLTISRLESEDFALYFCQYGTSLPTFGGKVEIK 128

Search completed: November 16, 2005, 22:01:54  
Job time : 59.9908 secs

CONFIDENTIAL (SECRET)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357A-34  
Perfect score: 556  
Sequence: 1 EIVMTSPATLSVSPGERAT.....CQYNNWPTFGQTKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520.5	93.6	117	4	US-09-203-768A-4
2	489	87.9	224	4	US-09-456-090A-82
3	489	87.9	224	4	US-09-456-090A-88
4	489	87.9	224	4	US-09-456-090A-90
5	489	87.9	224	4	US-09-453-234-82
6	489	87.9	224	4	US-09-453-234-88
7	489	87.9	224	4	US-09-453-234-90
8	486	87.4	224	4	US-09-456-090A-36
9	486	87.4	224	4	US-09-453-234-36
10	476	85.6	224	4	US-09-456-090A-84
11	476	85.6	224	4	US-09-453-234-84
12	475	85.4	224	4	US-09-456-090A-46
13	475	85.4	224	4	US-09-453-234-46
14	466	83.8	106	4	US-08-635-109-8
15	466	83.8	106	4	US-08-844-215-11
16	465.5	83.7	109	3	US-09-025-769B-16
17	465.5	83.7	109	4	US-09-490-070A-16
18	465.5	83.7	109	4	US-09-490-153-16
19	465.5	83.7	109	4	US-09-490-324-16
20	464.5	83.5	110	3	US-09-025-769B-30
21	464.5	83.5	110	3	US-09-025-769B-47
22	464.5	83.5	110	4	US-09-490-070A-30
23	464.5	83.5	110	4	US-09-490-070A-47
24	464.5	83.5	110	4	US-09-490-153-30
25	464.5	83.5	110	4	US-09-490-153-47
26	464.5	83.5	110	4	US-09-490-324-30
27	464.5	83.5	110	4	US-09-490-324-47

28 462 83.1 234 3 US-09-049-672A-6 Sequence 6, Appli  
29 459.5 82.6 235 4 US-09-472-087-14 Sequence 14, Appl  
30 459.5 82.6 235 4 US-09-472-087-65 Sequence 65, Appl  
31 457.5 82.3 108 2 US-08-232-081B-42 Sequence 42, Appl  
32 454.5 81.7 108 1 US-07-634-278-86 Sequence 86, Appl  
33 454.5 81.7 108 1 US-08-477-728-86 Sequence 86, Appl  
34 454.5 81.7 108 1 US-08-474-040-86 Sequence 86, Appl  
35 454.5 81.7 108 1 US-08-487-200-86 Sequence 86, Appl  
36 454.5 81.7 108 1 US-08-488-113B-150 Sequence 150, App  
37 454.5 81.7 108 2 US-08-477-484B-150 Sequence 150, App  
38 454.5 81.7 108 2 US-08-646-360-150 Sequence 150, App  
39 454.5 81.7 108 3 US-08-839-765-150 Sequence 150, App  
40 454.5 81.7 108 3 US-09-136-389-150 Sequence 150, App  
41 454.5 81.7 108 3 US-08-484-537-86 Sequence 86, Appl  
42 454.5 81.7 108 3 US-09-610-838-150 Sequence 150, App  
43 454.5 81.7 108 4 US-09-711-485-150 Sequence 150, App  
44 454 81.7 107 1 US-07-634-278-63 Sequence 63, Appl  
45 454 81.7 107 1 US-07-634-278-87 Sequence 87, Appl

#### ALIGNMENTS

RESULT 1

US-09-203-768A-4

; Sequence 4, Application US/09203768A

; Patent No. 6787638

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; APPLICANT: Watkins, Jeffrey D.

; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods

; TITLE OF INVENTION: of Use

; FILE REFERENCE: P-IX 2947

; CURRENT APPLICATION NUMBER: US/09/203,768A

; CURRENT FILING DATE: 1998-12-02

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 4

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-203-768A-4

Query Match 93.6%; Score 520.5; DB 4; Length 117;  
Best Local Similarity 93.5%; Pred. No. 5.6e-41;  
Matches 101; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 EIVMTSPATLSVSPGERATLSCRASQSSNNFAYVYQKPGQAPRLLIYGASTRATGIPA 60

DB 9 EIVMTSPATLSVSPGERATLSCRASQSSNNLAWYQKPGQAPRLLIYGASTRATGIPA 68

QY 61 RFSGSGSGTEFTLTISLSQSEDFAVYVYCOQYNNW-PRTFGQGTKEIK 107

DB 69 RFSGSGSGTEFTLTISLSQSEDFAVYVYCOQYNNWPPYTFGQGTKEIK 116

RESULT 2

US-09-456-090A-82

; Sequence 82, Application US/09456090A

; Patent No. 6680209

; GENERAL INFORMATION:

; APPLICANT: Buechler, Joe

; APPLICANT: Valkirs, Gunars

; APPLICANT: Gray, Jeff

; APPLICANT: Lonberg, Nils

; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS

; FILE REFERENCE: 020015-00020005

; CURRENT APPLICATION NUMBER: US/09/456,090A

; CURRENT FILING DATE: 1999-12-06

; NUMBER OF SEQ ID NOS: 110

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 82

; LENGTH: 224

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQQKPGQAPRLIFGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIYDASNRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQORTNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQQKPGQAPRLIFGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIYDASNRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQORTNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQQKPGQAPRLIFGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIYDASNRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQORTNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQQKPGQAPRLIFGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIYDASNRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQORTNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
US-09-453-234-88

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQQKPGQAPRLIFGASTRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIYDASNRATGIPA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQYNNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQORTNWPRTFGGTKVEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-453-234-88

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLIIFGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYCCQRTNWPRTFGGTKVEIK 107

RESULT 7
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Longberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match      87.9%; Score 489; DB 4; Length 224;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLIIFGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYCCQRTNWPRTFGGTKVEIK 107

RESULT 8
US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Longberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-1L
US-09-456-090A-36

Query Match      87.4%; Score 486; DB 4; Length 224;
Best Local Similarity 86.0%; Pred. No. 1.7e-37;
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLIIFGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYCCQRTNWPRTFGGTKVEIK 107

RESULT 9
US-09-453-234-36
; Sequence 36, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Longberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-36
US-09-453-234-36

Query Match      87.4%; Score 486; DB 4; Length 224;
Best Local Similarity 86.0%; Pred. No. 1.7e-37;
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLIIFGASTRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCOQNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLEPEDFAVYCCQRTNWPRTFGGTKVEIK 107

RESULT 10
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Longberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
```





```
; ADDRESSEE: REED & ROBINS
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,109
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCracken, Thomas P
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 2300-6146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-635-109-8

Query Match      83.8%; Score 466; DB 4; Length 106;
Best Local Similarity 83.7%; Pred. No. 5.4e-36;
Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 MTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLLIFGASTRATGIPARFS 63
Db 3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQQKPGQAPRLLIYGGNTRATGTPDRFS 62

QY 64 GSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 63 GSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 106

Search completed: November 16, 2005, 22:07:22
Job time : 19.1939 secs

; ADDRESSEE: REED & ROBINS
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,109
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCracken, Thomas P
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 2300-6146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-635-109-8

Query Match      83.8%; Score 466; DB 4; Length 106;
Best Local Similarity 83.7%; Pred. No. 5.4e-36;
Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 MTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLLIFGASTRATGIPARFS 63
Db 3 LTQSPATLSVSPGERASLSCRASQSVGNLAWYQQKPGQAPRLLIYGGNTRATGTPDRFS 62

QY 64 GSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 63 GSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 106

RESULT 15
US-08-844-215-11
; Sequence 11, Application US/08844215
; Patent No. 6747136
; GENERAL INFORMATION:
; APPLICANT: PERSON, MATS AXEL
; APPLICANT: ALLANDER, TOBIAS ERIK
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,215
; FILING DATE: 17-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/635,109
; FILING DATE: 19-APR-1996
```

המחלקה לבריאות הציבור  
המחלקה לבריאות הציבור

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 65.6949 Seconds  
(without alignments)  
681.481 Million cell updates/sec

Title: US-10-660-357A-34  
Perfect score: 556  
Sequence: 1 EIVMTQSPATLSVSPGERAT.....COQYNNWPRTFGQTKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications, AA.\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	107	14	US-10-330-613-34
2	556	100.0	107	14	US-10-330-530-34
3	556	100.0	107	16	US-10-660-357-34
4	546	98.2	107	14	US-10-330-613-6
5	546	98.2	107	14	US-10-330-530-6
6	546	98.2	107	16	US-10-660-357-6
7	534	96.0	107	15	US-10-251-085B-122
8	534	96.0	107	16	US-10-737-252-122
9	530	95.3	107	15	US-10-251-085B-126
10	530	95.3	107	16	US-10-737-252-126
11	527	94.8	107	15	US-10-251-085B-109

12	527	94.8	107	15	US-10-251-085B-123	Sequence 123, App
13	527	94.8	107	16	US-10-737-252-109	Sequence 109, App
14	527	94.8	107	16	US-10-737-252-123	Sequence 123, App
15	527	94.8	107	17	US-10-727-155-310	Sequence 310, App
16	527	94.8	107	17	US-10-727-155-313	Sequence 313, App
17	527	94.8	107	18	US-10-901-736-2	Sequence 2, Appli
18	525	94.4	107	15	US-10-251-085B-117	Sequence 117, App
19	525	94.4	107	16	US-10-737-252-117	Sequence 117, App
20	524.5	94.3	108	16	US-10-251-085B-132	Sequence 132, App
21	524.5	94.3	108	16	US-10-737-252-132	Sequence 132, App
22	524	94.2	107	15	US-10-251-085B-119	Sequence 119, App
23	524	94.2	107	16	US-10-737-252-119	Sequence 119, App
24	524	94.2	107	17	US-10-727-155-314	Sequence 314, App
25	524	94.2	107	17	US-10-938-353-107	Sequence 107, App
26	523.5	94.2	108	18	US-10-984-960A-29	Sequence 29, Appl
27	523	94.1	250	10	US-09-880-748-1952	Sequence 1952, Ap
28	523	94.1	250	15	US-10-293-418-1952	Sequence 1952, Ap
29	521	93.7	107	15	US-10-251-085B-115	Sequence 115, App
30	521	93.7	107	16	US-10-737-252-115	Sequence 115, App
31	520.5	93.6	117	14	US-10-300-675-4	Sequence 4, Appli
32	520.5	93.6	117	14	US-10-300-675-42	Sequence 42, Appl
33	520.5	93.6	117	14	US-10-300-675-44	Sequence 44, Appl
34	520.5	93.6	117	14	US-10-300-675-46	Sequence 46, Appl
35	520.5	93.6	117	17	US-10-910-124-4	Sequence 4, Appli
36	520	93.5	246	10	US-09-880-748-1268	Sequence 1268, Ap
37	520	93.5	246	15	US-10-293-418-1268	Sequence 1268, Ap
38	517	93.0	107	15	US-10-308-817-124	Sequence 124, App
39	517	93.0	107	15	US-10-453-698-124	Sequence 124, App
40	516	92.8	107	17	US-10-727-155-146	Sequence 146, App
41	516	92.8	107	17	US-10-727-155-184	Sequence 184, App
42	516	92.8	127	15	US-10-309-764-137	Sequence 137, App
43	515.5	92.7	106	17	US-10-727-155-277	Sequence 277, App
44	515	92.6	108	17	US-10-706-689-19	Sequence 19, Appl
45	515	92.6	108	18	US-10-988-360-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-34  
; Sequence 34, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-34

Query Match 100.0%; Score 556; DB 14; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.4e-40;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFWYQKPGQAPRLIFGASTRAIGIPA 60  
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFWYQKPGQAPRLIFGASTRAIGIPA 60  
QY 61 RFGSGSGTFTLTISLSQSEDFAVYVCOQYNNWPRTFGQTKVEIK 107  
Db 61 RFGSGSGTFTLTISLSQSEDFAVYVCOQYNNWPRTFGQTKVEIK 107

RESULT 2

```
US-10-330-530-34
; Sequence 34, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-34

Query Match      100.0%; Score 556; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 3
US-10-660-357-34
; Sequence 34, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-34

Query Match      100.0%; Score 556; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 4
US-10-330-613-6
; Sequence 6, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613-6

Query Match      98.2%; Score 546; DB 14; Length 107;
Best Local Similarity 97.2%; Pred. No. 1e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 5
US-10-330-530-6
; Sequence 6, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-6

Query Match      98.2%; Score 546; DB 14; Length 107;
Best Local Similarity 97.2%; Pred. No. 1e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQQKPGQAPRLIFGASTRATGIPA 60

QY 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107
Db 61 RFGSGSGTEFTLTISLSQSEDFAVYCCQYNNWPRTFGGTKVEIK 107

RESULT 6
US-10-660-357-6
; Sequence 6, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
```

```
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-6

Query Match
Best Local Similarity 98.2%; Score 546; DB 16; Length 107;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTEFTLTITSSLSQSEDFAVYVCOQYNNWPRFTGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLSQSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

RESULT 7
US-10-251-085B-122
; Sequence 122, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-122

Query Match
Best Local Similarity 96.0%; Score 534; DB 15; Length 107;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTEFTLTITSSLSQSEDFAVYVCOQYNNWPRFTGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLSQSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

RESULT 8
US-10-737-252-122
; Sequence 122, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
```

```
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-122

Query Match
Best Local Similarity 96.0%; Score 534; DB 16; Length 107;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTEFTLTITSSLSQSEDFAVYVCOQYNNWPRFTGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLSQSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

RESULT 9
US-10-251-085B-126
; Sequence 126, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-126

Query Match
Best Local Similarity 95.3%; Score 530; DB 15; Length 107;
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIINNFAVYQKPGQAPRLLIFGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 60
QY 61 RFGSGSGTEFTLTITSSLSQSEDFAVYVCOQYNNWPRFTGGTKVEIK 107
Db 61 RFGSGSGTEFTLTITSSLSQSEDFAVYVCOQYNNWPRFTGGTKVEIK 107

RESULT 10
US-10-737-252-126
; Sequence 126, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
```

```

; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-126

```

```

Query Match          95.3%; Score 530; DB 16; Length 107;
Best Local Similarity 94.4%; Pred. No. 2.5e-38;
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGTSTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107

```

```

RESULT 11
US-10-251-085B-109
; Sequence 109, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-109

```

```

Query Match          94.8%; Score 527; DB 15; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKRLEIK 107

```

```

RESULT 12
US-10-251-085B-123
; Sequence 123, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark

```

```

; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-123

```

```

Query Match          94.8%; Score 527; DB 15; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVDIK 107

```

```

RESULT 13
US-10-737-252-109
; Sequence 109, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-109

```

```

Query Match          94.8%; Score 527; DB 16; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAWYQKPGQAPRLLIYGASTRATGIPA 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLLIYGASTRATGIPA 60

QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKVEIK 107
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPRTFGGTKRLEIK 107

```

```

RESULT 14
US-10-737-252-123
; Sequence 123, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:

```

APPLICANT: Bowdish, Katherine S.  
APPLICANT: Frederickson, Shana  
APPLICANT: Renshaw, Mark  
APPLICANT: Lin, Ying-Chi  
APPLICANT: Maruyama, Toshiaki  
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION  
FILE REFERENCE: 1087-21 CIP  
CURRENT APPLICATION NUMBER: US/10/737,252  
CURRENT FILING DATE: 2003-12-15  
PRIOR APPLICATION NUMBER: US 10/251,085  
PRIOR FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: US 60/323,455  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 309  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 123  
LENGTH: 107  
TYPE: PRT  
ORGANISM: human  
US-10-737-252-123

Query Match 94.8%; Score 527; DB 16; Length 107;  
Best Local Similarity 93.5%; Pred. No. 4.5e-38;  
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQKPGQAPRLLIIFGASTRATGIPA 60  
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQKPGQAPRLLIIFGASTRATGIPA 60  
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYCCQYNNWPRTFGQGTKEIK 107  
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYCCQYNNWPRTFGQGTKEIK 107

RESULT 15

US-10-727-155-310  
Sequence 310, Application US/10727155  
Publication No. US2005004902A1  
GENERAL INFORMATION:  
APPLICANT: John S. Babcock  
APPLICANT: Jaspal S. Kang  
APPLICANT: Orit Foord  
APPLICANT: Larry Green  
APPLICANT: Xiao Feng  
APPLICANT: Scott Klakamp  
APPLICANT: Mary Haak-Frendscho  
APPLICANT: Palaniswami Rathanaswami  
APPLICANT: Craig Pigott  
APPLICANT: Meina Liang  
APPLICANT: Rozanne Lee  
APPLICANT: Kathy Manchulenchao  
APPLICANT: Raffaella Faggioni  
APPLICANT: Giorgio Senaldi  
APPLICANT: Qiaojuan Jane Su  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
FILE REFERENCE: ABGENIX.073A  
CURRENT APPLICATION NUMBER: US/10/727,155  
CURRENT FILING DATE: 2003-12-02  
PRIOR APPLICATION NUMBER: 60/430729  
PRIOR FILING DATE: 2002-12-02  
NUMBER OF SEQ ID NOS: 320  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 310  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-727-155-310

Query Match 94.8%; Score 527; DB 17; Length 107;  
Best Local Similarity 93.5%; Pred. No. 4.5e-38;  
Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQKPGQAPRLLIIFGASTRATGIPA 60  
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSIENNFAVYQKPGQAPRLLIIFGASTRATGIPA 60  
QY 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYCCQYNNWPRTFGQGTKEIK 107  
Db 61 RFSGSGSGTEFTLTITSSLSQSEDFAVYCCQYNNWPRTFGQGTKEIK 107

Search completed: November 16, 2005, 23:05:45  
Job time : 66.6949 secs

1111 1111 1111 (1111)



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:35:48 ; Search time 64.2353 Seconds  
(without alignments)  
674.351 Million cell updates/sec

Title: US-10-660-357A-38

Perfect score: 580

Sequence: 1 DIVWTQSPSLPVIQGPAS.....CMQALQIPITFGGKVKIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	580	100.0	112	7	ADC99809 Anti-huma
2	580	100.0	112	7	ADD05413 Anti-MUC1
3	580	100.0	112	7	ADF09851 Human ant
4	552	95.2	112	6	ABR55794 Kappa cha
5	552	95.2	112	6	ABR55786 Kappa cha
6	552	95.2	112	7	ADP03893 Murine-ex
7	548	94.5	262	5	ABP46070 Human Bly
8	548	94.5	262	7	ADG36887 Single ch
9	547	94.3	112	7	ADP03892 Murine-ex
10	546	94.1	239	3	AAY82615 Human PTH
11	545	94.0	112	6	ABR55770 Kappa cha
12	544	93.8	112	6	ABR55812 Kappa cha
13	544	93.8	112	8	ADI22119 Anti-plat
14	544	93.8	112	6	ADI22122 Anti-plat
15	540	93.1	112	6	ABR55796 Kappa cha
16	540	93.1	112	8	ADL93576 Human CD4
17	540	93.1	238	8	ADL93653 Human CD4
18	539.5	93.0	111	7	ADK18830 Anti-huma
19	539.5	93.0	111	7	ADK18796 Anti-huma
20	539.5	93.0	111	7	ADK18592 Anti-huma
21	539.5	93.0	111	7	ADK18855 Anti-huma
22	539.5	93.0	111	8	ADL25402 Human mab
23	539	92.9	112	8	ADL93564 Human CD4
24	539	92.9	238	8	ADL93649 Human CD4
25	538	92.8	112	7	ADJ76892 Anti-IGF-

ALIGNMENTS

RESULT 1

ADC99809

ID ADC99809 standard; protein; 112 AA.

XX ADC99809;

AC

XX 01-JAN-2004 (first entry)

DT

DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 38.

XX

KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human.

XX Homo sapiens.

XX

PN WO2003057838-A2.

XX

PD 17-JUL-2003.

XX

PF 26-DEC-2002; 2002WO-US041581.

XX

PR 28-DEC-2001; 2001US-0346299P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J;

XX

XX WPI; 2003-587113/55.

DR N-PSDB; ADC99811.

DR

PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease

PT or condition associated with expression of MUC18 in a patient, e.g.

PT tumors, cancers, and other malignancies.

XX

PS Claim 3; SEQ ID NO 38; 78pp; English.

XX

CC The invention relates to a novel isolated monoclonal antibody comprising

CC a heavy or light chain amino acid or a heavy or light chain variable

CC domain where the antibody binds to MUC18. The monoclonal antibody of the

CC invention demonstrates cytostatic activity and may be useful for treating

CC a disease or condition associated with the expression of MUC18 on the

CC cell surface such as tumours, specifically melanoma, oesophageal,

CC pancreatic or colorectal tumours, carcinomas, particularly cervical

CC carcinomas and cervical intraepithelial neoplasia and cancers including

CC colorectal, breast or lung cancer, as well as other malignancies. The

CC current sequence is that of the anti-human MUC18 monoclonal antibody

CC light chain protein of the invention.  
 XX  
 SQ Sequence 112 AA;

Query Match  
 Best Local Similarity 100.0%; Score 580; DB 7; Length 112;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
 DB 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112  
 DB 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112

RESULT 2  
 ADD05413  
 ID ADD05413 standard; protein; 112 AA.  
 XX  
 AC ADD05413;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-MUC18 antibody light chain variable region protein, SEQ ID NO 38.  
 XX  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; light chain.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057006-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041582.  
 XX  
 PR 28-DEC-2001; 2001US-0346460P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J, Bar-Eli M;  
 XX  
 DR WPI; 2003-577496/54.  
 DR N-PSDB; ADD05415.  
 XX  
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.  
 XX  
 Claim 3; SEQ ID NO 38; 87pp; English.

The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumour growth in an animal. The tumour inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody light chain, variable region,  
 CC protein of the invention.

XX  
 SQ Sequence 112 AA;

Query Match  
 Best Local Similarity 100.0%; Score 580; DB 7; Length 112;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
 DB 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112  
 DB 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112

RESULT 3  
 ADF09851  
 ID ADF09851 standard; protein; 112 AA.  
 XX  
 AC ADF09851;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human anti-MUC18 monoclonal antibody light chain #10.  
 XX  
 KW cell proliferation inhibition; MUC18 tumour antigen;  
 KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;  
 KW carcinoma; cancer; malignancy; light chain; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057837-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041580.  
 XX  
 PR 28-DEC-2001; 2001US-0346414P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-598367/56.  
 DR N-PSDB; ADF09853.  
 XX  
 XX Inhibiting cell proliferation associated with expression of MUC18 tumor  
 PT antigen, involves incubating and inhibiting cell by administering anti-  
 PT MUC18 monoclonal antibody.  
 XX  
 Claim 3; SEQ ID NO 38; 83pp; English.

The invention comprises a method for inhibiting cell proliferation  
 CC associated with expression of MUC18 tumour antigen. The method involves  
 CC administering anti-MUC18 monoclonal antibody. The method of the invention  
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)  
 CC proliferation associated with the expression of MUC18 tumour antigen, the  
 CC method is preferably useful for inhibiting tumour metastasis. The method  
 CC is useful for inhibiting cell proliferation in patients with tumours,  
 CC carcinomas, cancer and other malignancies. The present amino acid  
 CC sequence represents a light chain from an MUC18 tumour antigen-specific  
 CC monoclonal antibody.

XX  
 SQ Sequence 112 AA;

Query Match  
 Best Local Similarity 100.0%; Score 580; DB 7; Length 112;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
 DB 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112  
 DB 61 SGVPRFSGSGGTDTFTLKISRVEADDVGIIYCMQALQIPLTFGGGKVEIK 112

61 SGVPRFSGSGSDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112

Db

RESULT 4  
ID ABR55794 standard; protein; 112 AA.  
AC ABR55794;  
XX  
DT 02-SEP-2003 (first entry)  
DE Kappa chain variable region of anti-Ang-2 antibody 551 kappa.  
XX  
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;  
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;  
KW angiogenesis; antibody.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 23..40  
FT /note= "complementarity determining region (CDR) 1"  
FT Region 54..62  
FT /note= "complementarity determining region (CDR) 2"  
FT Region 93..102  
FT /note= "complementarity determining region (CDR) 3"  
XX  
PN WO2003030833-A2.  
XX  
XX 17-APR-2003.  
XX  
XX 11-OCT-2002; 2002WO-US032613.  
XX  
XX 11-OCT-2001; 2001US-0328604P.  
PR 10-OCT-2002; 2002US-00269805.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Oliner JD;  
PI  
XX WPI; 2003-504963/47.  
XX  
XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful  
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
XX  
PS Claim 1; Page 93; 161pp; English.  
XX  
XX The invention relates to a specific binding agent, which comprises at  
CC least one peptide selected from any of 62 peptides (ABR55794-830) or its  
CC fragment. The binding agents are antibodies that recognize and bind to  
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the  
CC antibody, is useful for inhibiting undesired angiogenesis, treating  
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
CC 2 activity, modulating vascular permeability or plasma leakage, or  
CC treating a disease (e.g. ocular neovascular disease, obesity,  
CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,  
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
CC disease, bone-related disease, or psoriasis) in a mammal. The present  
CC sequence represents a kappa chain variable region of an anti-Ang-2  
XX antibody  
XX  
SQ Sequence 112 AA;

Query Match 95.2%; Score 552; DB 6; Length 112;  
Best Local Similarity 94.6%; Pred. No. 2.3e-41;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DIVMTQSPVLPVPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60  
DB 1 DIVMTQSPVLPVPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60  
QY 61 SGVPRFSGSGSDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112

61 SGVPRFSGSGSDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112  
RESULT 5  
ID ABR55786 standard; protein; 112 AA.  
XX  
AC ABR55786;  
XX  
DT 02-SEP-2003 (first entry)  
DE Kappa chain variable region of anti-Ang-2 antibody 543 kappa.  
XX  
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;  
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;  
KW angiogenesis; antibody.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 23..40  
FT /note= "complementarity determining region (CDR) 1"  
FT Region 54..62  
FT /note= "complementarity determining region (CDR) 2"  
FT Region 93..102  
FT /note= "complementarity determining region (CDR) 3"  
XX  
PN WO2003030833-A2.  
XX  
XX 17-APR-2003.  
XX  
XX 11-OCT-2002; 2002WO-US032613.  
XX  
XX 11-OCT-2001; 2001US-0328604P.  
PR 10-OCT-2002; 2002US-00269805.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Oliner JD;  
PI  
XX WPI; 2003-504963/47.  
XX  
XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful  
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
XX  
PS Claim 1; Page 93; 161pp; English.  
XX  
XX The invention relates to a specific binding agent, which comprises at  
CC least one peptide selected from any of 62 peptides (ABR55786-830) or its  
CC fragment. The binding agents are antibodies that recognize and bind to  
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the  
CC antibody, is useful for inhibiting undesired angiogenesis, treating  
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
CC 2 activity, modulating vascular permeability or plasma leakage, or  
CC treating a disease (e.g. ocular neovascular disease, obesity,  
CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,  
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
CC disease, bone-related disease, or psoriasis) in a mammal. The present  
CC sequence represents a kappa chain variable region of an anti-Ang-2  
XX antibody  
XX  
SQ Sequence 112 AA;  
Query Match 95.2%; Score 552; DB 6; Length 112;  
Best Local Similarity 94.6%; Pred. No. 2.3e-41;  
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DIVMTQSPVLPVPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60  
DB 1 DIVMTQSPVLPVPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60  
QY 61 SGVPRFSGSGSDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112



RESULT 8  
ADG96897  
ID ADG96897 standard; protein; 262 AA.  
XX AC ADG96897;  
XX DT 11-MAR-2004 (first entry)  
XX DE Single chain antibody that immunospecifically binds BlyS SeqID 2081.  
XX KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;  
XX KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
XX KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
XX KW carcinoma; lymphoma; anti-rheumatic; anti-arthritis; neuroprotective;  
XX KW anti-inflammatory; anti-asthmatic; anti-allergic; cytostatic.  
XX OS Unidentified.  
XX PN WO2003055979-A2.  
XX PD 10-JUL-2003.  
XX PF 14-NOV-2002; 2002WO-US036496.  
XX PR 16-NOV-2001; 2001US-0331469P.  
XX PR 19-DEC-2001; 2001US-0340817P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;  
XX WPI; 2003-505530/47.  
XX DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
XX PT (BlyS), useful for detecting and treating diseases or disorders e.g.  
XX PT rheumatoid arthritis, asthma and leukemia.  
XX PS Example 1; SEQ ID NO 2081; 394pp; English.  
XX CC This invention relates to novel antibodies that immunospecifically bind  
XX CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to  
XX CC chromosome 13q34 and encodes a protein that is a member of the tumour  
XX CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
XX CC proliferation and differentiation. Specifically, it refers to single  
XX CC chain antibody molecules (scFvs) derived, preferably, from the variable  
XX CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
XX CC fragment thereof, of either human, murine, rat or monkey BlyS. The  
XX CC present invention refers to the use of such antibodies in various methods  
XX CC for the detection, diagnosis and prognosis of diseases related to the  
XX CC aberrant expression or inappropriate function of BlyS or its receptor. As  
XX CC such, these compositions are useful for identifying immune disorders  
XX CC including myasthenia gravis and multiple sclerosis, inflammatory  
XX CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
XX CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
XX CC lymphoma. Accordingly, they can be described as exhibiting various  
XX CC activities such as anti-rheumatic, anti-arthritis, neuroprotective,  
XX CC anti-inflammatory, anti-asthmatic, anti-allergic and cytostatic. This  
XX CC polypeptide sequence is a single chain antibody that binds BlyS of the  
XX CC invention. NOTE: The sequence data for this patent did not form part of  
XX CC the printed specification, but was obtained in electronic format  
XX CC directly from WIPO at ftp.wipo.int/pub/published pct\_sequences.  
XX SQ Sequence 262 AA;  
Query Match 94.5%; Score 548; DB 7; Length 262;  
Best Local Similarity 93.8%; Pred. No. 1.3e-40;  
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60  
DB 150 EIVMTQSPPLSLPVTPGEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 209

QY 61 SGVPRFRSGSGSGTDFTLKISRVEADDDGVIYYCMQALQIPLTFGGGKVEIK 112  
DB 210 SGVPRFRSGSGSGTDFTLKISRVEADDDGVIYYCMQALQIPLTFGGGKVEIK 261  
RESULT 9  
ADP03892  
ID ADP03892 standard; protein; 112 AA.  
XX AC ADP03892;  
XX DT 29-JUL-2004 (first entry)  
XX DE Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 32.  
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
XX KW cervical intraepithelial squamous neoplasia;  
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX KW gene therapy; murine; mouse; human; light chain variable domain.  
XX OS Unidentified.  
XX PN WO2003048328-A2.  
XX PD 12-JUN-2003.  
XX PF 02-DEC-2002; 2002WO-US038550.  
XX PR 03-DEC-2001; 2001US-0337275P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
XX PS Claim 3; SEQ ID NO 32; 89pp; English.  
XX CC The invention relates to a novel isolated monoclonal antibody (mAb)  
XX CC comprising a heavy chain polypeptide and light chain polypeptide having a  
XX CC sequence chosen from one of 53 fully defined amino acid sequences given  
XX CC in the specification, where the antibody specifically binds carbonic  
XX CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX CC demonstrates cytostatic activity and may be useful for treating a tumour,  
XX CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX CC tumour or breast cancer, possibly via gene therapy. The current sequence  
XX CC is that of a murine-expressed anti-human CA IX monoclonal antibody VL  
XX CC (light chain variable domain) protein of the invention. The protein was  
XX CC generated via the introduction of the human CA IX protein into a  
XX CC transgenic mouse strain.  
XX SQ Sequence 112 AA;  
Query Match 94.3%; Score 547; DB 7; Length 112;  
Best Local Similarity 93.8%; Pred. No. 6.4e-41;  
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60  
DB 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 60  
QY 61 SGVPRFRSGSGSGTDFTLKISRVEADDDGVIYYCMQALQIPLTFGGGKVEIK 112  
DB 61 SGVPRFRSGSGSGTDFTLKISRVEADDDGVIYYCMQALQIPLTFGGGKVEIK 112  
RESULT 10

AAy82615  
ID AAY82615 standard; protein; 239 AA.  
AC AAY82615;  
XX  
DT 02-AUG-2000 (first entry)  
XX  
DE Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.  
XX  
DE Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
XX hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;  
KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
KW antiarthritic; cytostatic; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 155  
FT /note= "possible Ala"  
XX  
PN JP2000080100-A.  
XX  
PD 21-MAR-2000.  
XX  
PF 12-OCT-1998; 98JP-00304793.  
XX  
PR 17-JUN-1998; 98JP-00188196.  
PR 26-JUN-1998; 98JP-00196729.  
XX  
XX (NIBS ) JAPAN TOBACCO INC.  
XX  
XX WPI; 2000-286723/25.  
DR N-PSDB; AAA13925.  
XX  
XX A human monoclonal antibody to parathyroid hormone related protein. -  
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
PT including metastasis, and pain.  
XX  
XX Claim 31; Page 45-46; 88pp; Japanese.  
XX  
XX The present invention describes a human monoclonal antibody to  
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
CC its fragments, following the stimulation of PTHrP has the following  
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
CC the release of calcium from bone; or (c) inhibits elevation of blood  
CC calcium content. The monoclonal antibody can be used in the treatment of  
CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome  
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
CC antiinflammatory activities. The present sequence represents a human  
CC PTHrP monoclonal antibody clone protein sequence from the present  
CC invention  
XX  
SQ Sequence 239 AA;  
  
Query Match 94.1%; Score 546; DB 3; Length 239;  
Best Local Similarity 93.8%; Pred. No. 1.8e-40;  
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 DIVVTQSPSLPVTGPGEPASISCRSSQSLQSGNNVLDWYLOKPGQSPOLLIVLGSNRA 60  
DB 21 DIVVTQSPSLPVTGPGEPASISCRSSQSLQSGNNVLDWYLOKPGQSPOLLIVLGSNRA 80  
  
QY 61 SGVDPDRFSGSGGTDFTLKISRVEADVGIYVCWQALQIPLTFGGGKVEIK 112  
DB 81 SGVDPDRFSGSGGTDFTLKISRVEADVGIYVCWQALQIPLTFGGGKVEIK 132  
  
RESULT 11  
ABR55770  
ID ABR55770 standard; protein; 112 AA.

XX  
AC ABR55770;  
XX  
DT 02-SEP-2003 (first entry)  
XX  
DE Kappa chain variable region of anti-Ang-2 antibody 526 kappa.  
XX  
KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;  
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;  
KW angiogenesis; antibody.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 23..46  
FT /note= "complementarity determining region (CDR) 1"  
FT Region 54..62  
FT /note= "complementarity determining region (CDR) 2"  
FT Region 93..102  
FT /note= "complementarity determining region (CDR) 3"  
XX  
PN WO2003030833-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 11-OCT-2002; 2002WO-US032613.  
XX  
PR 11-OCT-2001; 2001US-0328604P.  
PR 10-OCT-2002; 2002US-00269805.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Oliner JD;  
XX  
XX WPI; 2003-504963/47.  
DR  
XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful  
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
XX  
XX Claim 1; Page 93; 161pp; English.  
XX  
XX The invention relates to a specific binding agent, which comprises at  
CC least one peptide selected from any of 62 peptides (ABR55769-830) or its  
CC fragment. The binding agents are antibodies that recognize and bind to  
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the  
CC antibody, is useful for inhibiting undesired angiogenesis, treating  
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
CC 2 activity, modulating vascular permeability or plasma leakage, or  
CC treating a disease (e.g. ocular neovascular disease, obesity,  
CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,  
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
CC disease, bone-related disease, or psoriasis) in a mammal. The present  
CC sequence represents a kappa chain variable region of an anti-Ang-2  
CC antibody  
XX  
SQ Sequence 112 AA;  
  
Query Match 94.0%; Score 545; DB 6; Length 112;  
Best Local Similarity 93.8%; Pred. No. 9.7e-41;  
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 DIVVTQSPSLPVTGPGEPASISCRSSQSLQSGNNVLDWYLOKPGQSPOLLIVLGSNRA 60  
DB 1 DIVVTQSPSLPVTGPGEPASISCRSSQSLQSGNNVLDWYLOKPGQSPOLLIVLGSNRA 60  
  
QY 61 SGVDPDRFSGSGGTDFTLKISRVEADVGIYVCWQALQIPLTFGGGKVEIK 112  
DB 61 SGVDPDRFSGSGGTDFTLKISRVEADVGIYVCWQALQIPLTFGGGKVEIK 112  
  
RESULT 12  
ABR55812







PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.

XX PS  
XX Claim 1; Page 93; 161pp; English.

XX CC The invention relates to a specific binding agent, which comprises at  
CC least one peptide selected from any of 62 peptides (ABR5769-830) or its  
CC fragment. The binding agents are antibodies that recognize and bind to  
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the  
CC antibody, is useful for inhibiting undesired angiogenesis, treating  
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
CC 2 activity, modulating vascular permeability or plasma leakage, or  
CC treating a disease (e.g. ocular neovascular disease, obesity,  
CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,  
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
CC disease, bone-related disease, or psoriasis) in a mammal. The present  
CC sequence represents a kappa chain variable region of an anti-Ang-2  
XX antibody

SQ Sequence 112 AA;

Query Match 93.1%; Score 540; DB 6; Length 112;  
Best Local Similarity 92.0%; Pred. No. 2.7e-40;  
Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIWVTQSPSLPVTGPGEASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRA 60

DB 1 DIWVTQSPSLPVTGPGEASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEADGVYICMQALQIPLTFGGSKVEIK 112

DB 61 SGVPDRFSGSGGTDFTLKISRVEADGVYICMQALQIPLTFGGSKVEIK 112

Search completed: November 16, 2005, 21:51:43  
Job time : 64.2353 secs

THE HOUSE OF COMMONS

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:37:48 ; Search time 13.3824 Seconds  
(without alignments)  
805.260 Million cell updates/sec

Title: US-10-660-357A-38  
 Perfect score: 580  
 Sequence: 1 DIWNTQSPLSLPIVPGEPAS.....CMOALQIPLTFGGGTTKVEIK 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database :      PIR_79:*
1:  _pir1:*
2:  _pir2:*
3:  _pir3:*
4:  _pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	550	94.8	125	2	S40356	Ig kappa chain - h
2	546	94.5	112	2	S58206	Ig light chain v r
3	538	92.8	112	2	S58207	Ig light chain v r
4	538	92.8	132	2	S26882	Ig kappa chain v r
5	538	92.8	135	2	S40342	Ig kappa chain - h
6	538	92.8	136	2	S40357	Ig kappa chain v-J
7	526	90.7	117	1	K2HUGM	Ig kappa chain pre
8	519.5	89.6	126	2	S40339	Ig kappa chain - h
9	512.5	88.4	112	1	K2HUML	Ig kappa chain v-I
10	505	87.1	131	2	S40372	Ig kappa chain v-J
11	501	86.4	113	1	K2HUTW	Ig kappa chain v-I
12	501	86.4	121	2	S40371	Ig kappa chain - h
13	490	84.5	124	2	S03876	Ig kappa chain v-I
14	487	84.0	123	2	S40319	Ig kappa chain v r
15	478.5	82.5	130	2	S40321	Ig kappa chain - h
16	478	82.4	100	2	S24681	Ig kappa chain - h
17	474.5	81.8	115	1	K2HUCM	Ig kappa chain v-I
18	470	81.0	112	2	F27887	Ig kappa chain v r
19	468	80.7	114	2	S40375	Ig kappa chain - h
20	465.5	80.3	126	2	S40341	Ig kappa chain - h
21	465	80.2	112	2	B27887	Ig kappa chain v r
22	465	80.2	115	2	S38715	Ig kappa chain v r
23	464	80.0	112	2	S38719	Ig light chain v r
24	463	79.8	112	2	E27887	Ig kappa chain v r
25	463	79.8	131	2	D29380	Ig kappa chain pre
26	463	79.8	219	2	S52028	Ig kappa chain - m
27	462	79.7	112	2	S53750	antibody Fab Jcl 1
28	462	79.7	131	2	PT0359	Ig kappa chain v r
29	462	79.7	118	2	B34904	Ig kappa chain pre

## RESULT 1

S40356  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40356  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40356  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
A:Cross-references: EMBL:X72466; NID:G441400; PID:CA51134.1; PID:G441401  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:25-104/Domain: immunoglobulin homology <IMW>

Query Match	94.8%	Score 550	DB 2	Length 125
Best Local Similarity	93.8%	Pred. No. 9.3e-46		
Matches 10	Conservative	3	Mismatches 4	Indels 0
Gaps 0				
Qy	1	DIVMTQSPFLSLPVI	GPSPASISCRSSOSLQSGNNYLDWY	LQKPGQSPOLLIIYLGSNRA 60
			:	:
Db	10	DIVMTQSPFLSLPVT	GPSPASISCRSSOSLHHNGYNYLDWY	LQKPGQSPOLLIIYLGSNRA 69
			:	:
Qy	61	SGVPDRFSGSGSGTD	FTLKISRVEADPVGYICWQAQIPLT	FGGGTKVEIK 112
			:	:
Db	70	SGVPDRFSGSGSGTD	FTLKISRVEADPVGYICWGLVLOIPLT	FGGGTKVEIK 121
			:	:

## RESULT 2

S58206  
Ig light chain V region anti-F(ab')2 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000  
C/Accession: S58206  
R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.  
submitted to the EMBL Data Library, July 1995  
A/Description: Characterisation of heavy and light chain immunoglobulin var  
A/Reference number: S58206  
A/Accession: S58206  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-112 <WEL>  
A/Cross-references: EMBL:X89054; NID:G929640; PIDN:CAA61441.1; PID:G929641  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 94.5%; Score 548; DB 2; Length 112;

```
Best Local Similarity 93.8%; Pred. No. 1.3e-45;
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
Db 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHGNYNYFDWYLOKPGSQSPQLLIYLGNSRA 60

QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112

RESULT 3
S59207
IG kappa chain V region anti-F(ab')2 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C;Accession: S58207
R;Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling,
submitted to the EMBL Data Library, July 1995
A;Description: Characterization of heavy and light chain immunoglobulin variable region
A;Reference number: S58206
A;Accession: S58207
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-112 <HEL>
A;Cross-references: EMBL:X99056; NID:g929642; PIDN:CAA61443.1; PID:g929643
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 538; DB 2; Length 112;
Best Local Similarity 92.9%; Pred. No. 1.2e-44;
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
Db 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHGNYNYLDWYLOKPGSQSPQLLIYLGNSRA 60

QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112

RESULT 4
S26882
IG kappa chain V region (V607) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: S26882
R;Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combratio, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A;Title: Megabase inversions in the human genome as physiological events.
A;Reference number: S26882; MUID:90370099; PMID:2118596
A;Accession: S26882
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-132 <WEI>
A;Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 538; DB 2; Length 132;
Best Local Similarity 92.9%; Pred. No. 1.4e-44;
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
Db 21 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHGNYNYLDWYLOKPGSQSPQLLIYLGNSRA 80

QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
Db 81 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 132

RESULT 7
K2HUGM
IG kappa chain precursor V-II region (GM607) - human (fragment)
C;Species: Homo sapiens (man)
```

```
QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
Db 81 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 132

RESULT 5
S40342
IG kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S40342
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40342
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-135 <KLE>
A;Cross-references: UNIPROT:Q8NEK0; EMBL:X72452; NID:g441372; PID:g441373
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;29-108/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 538; DB 2; Length 135;
Best Local Similarity 92.9%; Pred. No. 1.4e-44;
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
Db 14 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHGNYNYLDWYLOKPGSQSPQLLIYLGNSRA 73

QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
Db 74 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 125

RESULT 6
S40357
IG kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S40357
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40357
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-136 <KLE>
A;Cross-references: UNIPROT:Q8NEK0; EMBL:X72467
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 538; DB 2; Length 136;
Best Local Similarity 92.9%; Pred. No. 1.4e-44;
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLQSGNNYLDWYLOKPGSQSPQLLIYLGNSRA 60
Db 21 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHGNYNYLDWYLOKPGSQSPQLLIYLGNSRA 80

QY 61 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 112
Db 81 SGVPRDFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGTKVEIK 132

RESULT 7
K2HUGM
IG kappa chain precursor V-II region (GM607) - human (fragment)
C;Species: Homo sapiens (man)
```

C; Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
C; Accession: A01889; B24452  
R; Klobeck, H.G.; Solomon, A.; Zachau, H.G.  
Nature 309, 73-76, 1984  
A; title: Contribution of human V-kappaII germ-line genes to light-chain div  
A; Reference number: A01889; MUID:84191506; PMID:6325927

A/Accession: A01889  
A/Molecule type: mRNA  
A/Residues: 1-117 <KLO>  
A/Cross-references: UNIPROT:P06309  
A/Note: the sequence was determined from the differentiated gene  
C/Genetics:  
A/Gene: GDB:IGKV2  
A/Cross-references: GDB:136265  
A/Map position: 2p12-2p12  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/1-4/Domain: signal sequence (fragment) #status predicted <SIG>  
F/5-11/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>  
F/20-99/Domain: immunoglobulin homology <IMM>  
F/27-97/Disulfide bonds: #status predicted

Query Match	90.7%	Score 526;	DB 1;	Length 117;
Best Local Similarity	91.1%	Pred. NO. 1.7e-43;		
Matches 102;	Conservative	2;	Mismatches 8;	Indels 0;
Gaps	0;			

<b>Qy</b>	1	DIVMTQSPILPVI	GPEPASISCRSSQLSQNGNYYLDWYLRKPGQSPOLLIIYGSNRA	60
<b>Dd</b>	5	DIVMTQSPILPVT	GPEPASISCRSSQLSHSGNYLDWYLRKPGQSPOLLIIYGSNRA	64

Qy 61 SGVPDRFSGSGSDFTLKISRVEADDDGIVYYCMQALQIPLTFGGGTKVEIK 112  
 |||||  
 pb 65 SGVPDRFSGSGSDFTLKISRVEADDDGIVYYCMQGLPOTFGGGTKVEIK 116  
 |||||

RESULT 8  
S40339  
IG kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40339  
R; Klein, R.; Jaenichen, R.; Zachau, H. G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40339  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-126 <KLE>  
A:Cross-references: EMBL:X72449; NID:G441366; PIDN:CAAS1117.1; PID:G441367  
C:Superfamily: immunoglobulin v region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-110/Domain: immunoglobulin homology <IMM>

Query Match	89.6%	Score 519.5;	DB 2;	Length 126;
Best Local Similarity	91.1%;	Pred. No. 7.9e-43;		
Matches 102: Conservative	3;	Mismatches 6;	Indels 11;	Gaps 1;

Qy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Qy	1	D	I	V	M	T	Q	S	P	L	S	L	P	V	I	P	G	E	P	A	S	T	C	R	S	S	Q	S	L	Q	S	N	G	N	N	Y	L	D	W	Y	L	K	P	G	Q	S	P	O	L	L	I	Y	G	S	N	R	A	60		
Dy	16	D	I	V	M	T	Q	S	P	L	S	L	P	V	I	P	G	E	P	A	S	T	C	R	S	S	Q	S	L	Q	S	N	G	N	N	Y	L	D	W	Y	L	K	P	G	Q	S	P	O	L	L	I	Y	G	S	N	R	A	75		

Qy	61	SGVPDRFSGSGGTFTLKISRVEADVGVIYCMQALQPLTFGGGTKVEIK	112
		:     :     :     :     :     :     :	
Db	76	SGVPDRFSGSGGTFTLKISRVEADVGVIYCMQALQPLTFGGGTKVEIK	126

RESULT 9  
K2HUML  
Ig kappa chain V-II region (Mil) - human (tentative sequence)  
C:Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C;Accession: A01887  
R;Dreyer, W.J.; Gray, W.R.; Hood, L.  
Cold Spring Harb. Symp. Quant. Biol. 32, 353-367, 1967  
A;Title: The genetic, molecular, and cellular basis of antibody formation:  
A;Reference number: A01887  
A;Accession: A01887  
A;Molecule type: protein  
A;Residues: 1-112 <DR>  
A;Cross-references: UNIPROT:P01616  
A;Note: The C region of this chain has the Inv (3) marker  
C;Comment: This is a Bence Jones protein.

C; Gene: IGHV2  
A; Gene: GDB:IGKV2  
C; Gene: IGHV2  
A; Cross-references: GDB:136265  
A; Map position: 2p12-2p12  
C; Complex: An immunoglobulin heterotrimer consists of two identical light chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate in a heterotrimer.  
C; Superfamily: immunoglobulin V region; immunoglobulin homology  
C; Keywords: heterotrimer  
F; 16-94/Domain: immunoglobulin homology <IMV>  
F; 23-92/Disulfide bonds: #status predicted

Query Match	88.4%	Score 512.5;	DB 1;	Length 112;
Best Local Similarity	83.9%	Pred. No. 3.2e-42;		
Matches	94:	Conservative	14:	Mismatches 3;
				Indels 11;
				Gaps 1;

Qy 1 DIVMTQSPISL PVI PCEPASISCRSSQSLQSGNGNVIDWYLOKPGQSPQLLIYLSNRA 60

Dp 1 DIVLTQSPISL PVTCEPASISCRSSONLLZSBG-BYLDWYLPKPGZSPQLLIYLSNRA 59

Qy	61	SGVDRFSGSGTFTLKISRVEADVGIIYCMQALQIPLTFGGGKVEIK	112
		:     :     :     :     :     :	
Dp	60	SGVNRFSGSGGTFTLKISRVAZGVVYCMQALQIPLTFGGGNNVEIK	111

## RESULT 10

S40372  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40372  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40372  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-131 <KLE>  
A:Cross-references: EMBL:X72482; NTD:g441432; PIDN:CAAS1150.1; PID:g441433  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match	87.1%	Score 505;	DB 2;	Length 131;
Best Local Similarity	86.5%;	Pred. No. 2e-41;		
Matches 96;	Conservative	6;	Mismatches 9;	Indels 0;
Gaps	0;			

[illegible]

QY 61 SGVPDRFSGSGGDTFLKISRVEADDDGVIYCMQALQIPLTFGGTKVEI 111  
 |||||  
 81 SGVPDRFSGSGGDTFLKISRVEADDDGVIYCMQALQIPLTFGGTKVEI 131  
 |||||

## RESULT 11

Ig kappa chain V-II region (Tew) - human (tentative sequence)  
 C/Species: Homo sapiens (man)  
 C/Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text change 09-Jul-2004  
 K2HUTW





THE UNIVERSITY OF CHICAGO  
LIBRARY



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:36:13 ; Search time 62.7941 Seconds  
(without alignments)  
913.348 Million cell updates/sec

Title: US-10-660-357A-38  
Perfect score: 580  
Sequence: 1 DIVMTQSPSLPVIQEPAS.....CMQALQIPITFGGTRKVEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	90.9	239	2 Q8NEK0	Q8nek0 homo sapien
2	526	90.7	117	1 KV2E_HUMAN	P06309 homo sapien
3	512.5	88.4	112	1 KV2C_HUMAN	P01616 homo sapien
4	502.5	86.6	240	2 Q6PIH6	Q6pih6 homo sapien
5	501	86.4	113	1 KV2D_HUMAN	P01617 homo sapien
6	474.5	81.8	115	1 KV2A_HUMAN	P01614 homo sapien
7	456	78.6	248	2 Q65ZQ7	Q65zq7 mus sp. b3 (
8	455	78.4	113	1 KV2B_HUMAN	P01615 homo sapien
9	455	78.4	113	1 KV2G_MOUSE	P01631 mus musculus
10	444	76.6	133	1 KV2F_HUMAN	P06310 homo sapien
11	444	76.6	219	2 Q65ZC0	Q65zc0 mus musculus
12	440	75.9	239	2 Q6F491	Q6f491 homo sapien
13	439	75.7	239	2 Q8TCD0	Q8tcd0 homo sapien
14	429	74.0	113	1 KV2F_MOUSE	P01630 mus musculus
15	427	73.6	113	1 KV2E_MOUSE	P03976 mus musculus
16	426.5	73.5	114	2 Q9UL80	Q9ul80 homo sapien
17	424	73.1	112	2 Q6LEM8	Q6lem8 mus musculus
18	420	72.4	112	1 KV2D_MOUSE	P01629 mus musculus
19	406	70.0	113	1 KV2C_MOUSE	P01628 mus musculus
20	404	69.7	112	1 KV2A_MOUSE	P01626 mus musculus
21	397.5	68.5	108	1 KV1_CANFA	P01618 canis famil
22	387.5	66.8	134	1 KV4C_HUMAN	P06314 homo sapien
23	385	66.4	133	1 KV4B_HUMAN	P06313 homo sapien
24	378.5	65.3	114	1 KV4A_HUMAN	P01625 homo sapien
25	376.5	64.9	255	2 Q6KB05	Q6kb05 mus musculus
26	374	64.5	109	2 Q9UL78	Q9ul78 homo sapien
27	371	64.0	120	1 KV2B_MOUSE	P01627 mus musculus
28	365	62.9	109	1 KV3B_HUMAN	P01620 homo sapien
29	365	62.9	235	2 Q6GMV9	Q6gmrv9 homo sapien
30	364	62.8	109	1 KV3D_HUMAN	P01622 homo sapien
31	362.5	62.5	111	1 KV3H_MOUSE	P01660 mus musculus

#### RESULT 1

ID	Q8NEK0	PRELIMINARY;	PRT;	239 AA.
AC	Q8NEK0;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC030814; AAH30814.1; -.			
DR	PIR; S23638; S23638.			
DR	PIR; S34091; S34091.			
DR	PIR; S40342; S40342.			
DR	PIR; S40357; S40357.			
DR	HSSP; P01834; I172.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_c1.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			

32	359.5	62.0	111	2 Q920E9	Q920e9 mus musculus
33	359	61.9	129	1 KV3L_HUMAN	P18135 homo sapien
34	358.5	61.8	111	1 KV3R_MOUSE	P01670 mus musculus
35	357.5	61.6	111	1 KV3U_MOUSE	P01673 mus musculus
36	357	61.6	129	1 KV3M_HUMAN	P18136 homo sapien
37	356.5	61.5	111	1 KV3J_MOUSE	P01662 mus musculus
38	356.5	61.5	111	1 KV3S_MOUSE	P01671 mus musculus
39	355.5	61.3	131	1 KV3I_MOUSE	P01661 mus musculus
40	355	61.2	109	1 KV3E_HUMAN	P01623 homo sapien
41	353.5	60.9	111	1 KV4D_HUMAN	P83593 homo sapien
42	353.5	60.9	111	1 KV3K_MOUSE	P01663 mus musculus
43	353.5	60.9	111	1 KV3L_MOUSE	P01664 mus musculus
44	352.5	60.8	111	1 KV3C_MOUSE	P01656 mus musculus
45	352.5	60.8	111	1 KV3N_MOUSE	P01666 mus musculus

#### ALIGNMENTS



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN NCBI\_TaxID=9606;  
 (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwen P.J., Ketterman K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RP "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034142; AAH34142.1; -;  
 DR HSSP; P01837; 1KB5.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig.C1.  
 DR InterPro; IPR003006; Ig.MHC.  
 DR InterPro; IPR003596; Ig.V.  
 DR Pfam; PF07654; C1-set; I.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 240 AA; 26234 MW; 18804D8B8B781EC4 CRC64;  
 Query Match 86.6%; Score 502.5; DB 2; Length 240;  
 Best Local Similarity 87.6%; Pred. No. 2.2e-44;  
 Matches 99; Conservative 3; Mismatches 10; Indels 1; Gaps 1;  
 QY 1 DIVMTQSLPLSVIPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPOLLIVYLSNRA 60  
 DB 21 DIVMAQSPULSVTPGEPASISCRSSQSLHSGNNGYLDWYLOKPGQSPOLLIVYLSNRA 80  
 QY 61 SGVPRFSGSGGTDTFTLKISRVEADVDGIYCMQALQI-PLTFGGGKVEIK 112  
 DB 81 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQALQTPPYTFGGGKLEIK 133  
 RESULT 5  
 KV2D HUMAN  
 ID KV2D HUMAN STANDARD; PRT; 113 AA.  
 AC P01617;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-II region TEW.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN NCBI\_TaxID=9606;

RN SEQUENCE (BENCE-JONES PROTEIN TEW).  
 RP MEDLINE=74148480; PubMed=4596149;  
 RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;  
 RT "Amino acid sequence of a kappa Bence Jones protein from a case of  
 RT primary amyloidosis";  
 RL Biochemistry 12:3763-3780 (1973).  
 RN [2]  
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).  
 RX MEDLINE=73166638; PubMed=4700495;  
 RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,  
 RA Glenner G.G.;  
 RT "Structural identity of Bence Jones and amyloid fibril proteins in a  
 RT patient with plasma cell dyscrasia and amyloidosis.";  
 RL J. Clin. Invest. 52:1276-1281 (1973).  
 CC -!- MISCELLANEOUS: The major amyloid protein appears to be identical  
 CC with the Bence Jones protein isolated from the same patient.  
 CC -!- MISCELLANEOUS: This protein was isolated from the urine of a  
 CC patient with plasma cell dyscrasia and amyloidosis.  
 CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
 CC marker.  
 CC PIR; A30370; K2HUTW.  
 DR HSSP; Q99M37; 1191.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; F:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR Amyloid; Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 39  
 FT DOMAIN 40 54  
 FT DOMAIN 55 61  
 FT DOMAIN 62 93  
 FT DOMAIN 94 102  
 FT DOMAIN 103 112  
 FT DISULFID 23 93  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12316 MW; 0C3C8F81F1843CA CRC64;  
 Query Match 86.4%; Score 501; DB 1; Length 113;  
 Best Local Similarity 84.8%; Pred. No. 1.3e-44;  
 Matches 95; Conservative 10; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 DIVMTQSLPLSVIPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPOLLIVYLSNRA 60  
 DB 1 DIVMTQSLPLSVTPGEPASISCRSSQSLHSGNNGYLDWYLOKPGQSPOLLIVYLSNRA 60  
 QY 61 SGVPRFSGSGGTDTFTLKISRVEADVDGIYCMQALQIPLTFGGGKVEIK 112  
 DB 61 SGVPRFSGSGGTDTFTLKISRVEADVGVIYCMQALQAPITFGGQTRLEIK 112  
 RESULT 6  
 KV2A HUMAN  
 ID KV2A HUMAN STANDARD; PRT; 115 AA.  
 AC P01614;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-II region Cum.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=68242259; PubMed=5586923;  
 RA Hilschmann N.;

RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
 RN [2]

RP REVISIONS TO 50; 52; 96 AND 97.  
 RX MEDLINE=70063440; PubMed=4188189;  
 RA Hilschmann N.;  
 RT "Molecular basis of antibody formation.";  
 RL Naturwissenschaften 56:195-205(1969).  
 CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; B91639; K2HUCM.  
 DR HSSP; P01751; 1NOB.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin V region.  
 FT DISULFID 24 95 By similarity.  
 FT NON TER 115 115  
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 81.8%; Score 474.5; DB 1; Length 115;  
 Best Local Similarity 82.3%; Pred. No. 7.7e-42;  
 Matches 93; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVMTQSPFLSPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNR 59  
 DB 2 DIVMTQSPFLSPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLTSTR 61  
 QY 60 ASGVPRFRFGSGSGTDTFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 112  
 DB 62 ASGVPRFRFGSGSGTDTFTLKISRVAEDGVYICMQRLPIPTFGGQTKLEIR 114

RESULT 7  
 Q65ZQ7 PRELIMINARY; PRT; 248 AA.  
 ID Q65ZQ7  
 AC Q65ZQ7  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE B3(Fv)-PE40 (Fragment).  
 GN Name=B3(Fv)-PE40;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=92020904; PubMed=1924323;  
 RA Brinkmann U., Bai L.H., FitzGerald D.J., Willingham M., Pastan I.;  
 RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete regression of a human carcinoma in mice."  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).  
 DR EMBL; S57990; AAB19971.2; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IGV; 2.  
 DR SMART; SM00406; IGV; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 FT NON TER 248 248  
 SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 78.6%; Score 456; DB 2; Length 248;  
 Best Local Similarity 75.9%; Pred. No. 1.7e-39;

Matches 85; Conservative 12; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 DIVMTQSPFLSPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
 DB 136 DIVMTQSPFLSPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYKVSNR 195  
 QY 61 SGVPRFRFGSGSGTDTFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 112  
 DB 196 SGVPRFRFGSGSGTDTFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 247

RESULT 8  
 KV2B HUMAN  
 ID KV2B HUMAN STANDARD; PRT; 113 AA.  
 AC P01615;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-II region FR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=76253627; PubMed=821524;  
 RA Riessen W.F., Jaton J.-C.;  
 RT "Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine."  
 RL Biochemistry 15:3829-3833(1976).  
 CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.

DR PIR; A01886; K2HUPR.  
 DR HSSP; Q99M37; 1I91.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 39 Complementarity-determining-1.  
 FT DOMAIN 40 54 Framework-2.  
 FT DOMAIN 55 61 Complementarity-determining-2.  
 FT DOMAIN 62 93 Framework-3.  
 FT DOMAIN 94 102 Complementarity-determining-3.  
 FT DOMAIN 103 112 Framework-4.  
 FT DISULFID 23 93 By similarity.  
 FT NON TER 113 113  
 SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB968E CRC64;

Query Match 78.4%; Score 455; DB 1; Length 113;  
 Best Local Similarity 75.0%; Pred. No. 8.3e-40;  
 Matches 84; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIVMTQSPFLSPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
 DB 1 DVVMTQSPFLSPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYSSYRD 60  
 QY 61 SGVPRFRFGSGSGTDTFTLKISRVEADDVGIYCMQALQIPLTFGGGTVKEIK 112  
 DB 61 SGVPRFRFGSGSGTDTFTLKISRVAEDGVYICMQATZSPYTFGGQTKLZIK 112

RESULT 9  
 KV2G MOUSE  
 ID KV2G MOUSE STANDARD; PRT; 113 AA.  
 AC P01631;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

```

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
CC protein that binds digoxin.
CC PIR; A01914; KVM526.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Monoclonal antibody.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 78.4%; Score 455; DB 1; Length 113;
Best Local Similarity 77.7%; Pred. No. 8.3e-40;
Matches 87; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLSPVLPGEPAISCRSSQSLQSGNNYLDWYLQKPGQSPQLLIYLGNSRA 60
Db 1 DVVMTQSPSLSPVLPGEPAISCRSSQSLVHSGNTYLNWYLQKAGQSPKLLIYKVSNR 60

QY 61 SGVPRDFSGSGGTDFTLKISRVEADVGIYCYMQALQIPLTFGGGTKEIK 112
Db 61 SGVPRDFSGSGGTDFTLKISRVEADLIYFCSTHTVPPPTFGGTKEIK 112

RESULT 10
KV2F HUMAN STANDARD; PRT; 133 AA.
AC P06310.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Kloeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

---

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00020; CAA77315.1; -.
DR PIR; A01890; K2HURP.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-II region RPMI 6410.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 59 Complementarity-determining-1.
FT DOMAIN 60 74 Framework-2.
FT DOMAIN 75 81 Complementarity-determining-2.
FT DOMAIN 82 113 Framework-3.
FT DOMAIN 114 122 Complementarity-determining-3.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 113 By similarity.
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 76.6%; Score 444; DB 1; Length 133;
Best Local Similarity 76.8%; Pred. No. 1.4e-38;
Matches 86; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLSPVLPGEPAISCRSSQSLQSGNNYLDWYLQKPGQSPQLLIYLGNSRA 60
Db 21 DVVMTQSPSLSPVLPGEPAISCRSSQSLVSDGNTYLNWYFQRFQSPRRLLIYKVSNRD 80

QY 61 SGVPRDFSGSGGTDFTLKISRVEADVGIYCYMQALQIPLTFGGGTKEIK 112
Db 81 SGVPRDFSGSGGTDFTLKISRVEADVGVYCYMQGTHTSWTFTGGGTKEIK 132

RESULT 11
Q65ZC0 PRELIMINARY; PRT; 219 AA.
ID Q65ZC0;
AC Q65ZC0;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Kappa light chain C_region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chi t I.";
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL; Z37499; CAA85724.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.

```

```
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 219 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;
Query Match 76.6%; Score 444; DB 2; Length 219;
Best Local Similarity 75.0%; Pred. No. 2.6e-38;
Matches 84; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
QY 1 DIVMTQSPSLSPVTPGPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYIGSNRA 60
DB 1 ELVMTQSPSLSVSLGDAQISCRSSQSLVHTNGTYLHWYLOKGLSPKLLIYVSNRF 60
QY 61 SGVPRFSGSGGTFTLKISRVEADDDGIYCYMQALQIPLTFGGGTKEIK 112
DB 61 SGVPRFSGSGGTFTLKISRVEADDDGIYCYMQALQIPLTFGGGTKEIK 112
RESULT 12
Q6P491
ID Q6P491 PRELIMINARY; PRT; 239 AA.
AC Q6P491
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063599; AAH63599.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
```

```
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
Query Match 75.9%; Score 440; DB 2; Length 239;
Best Local Similarity 75.9%; Pred. No. 7.7e-38;
Matches 85; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
QY 1 DIVMTQSPSLSPVTPGPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYIGSNRA 60
DB 21 DIVMTQSPSLSPVTLGQAPASISCRSSQSLVHTNGTYLHWYLOKGLSPKLLIYKISNRF 80
QY 61 SGVPRFSGSGGTFTLKISRVEADDDGIYCYMQALQIPLTFGGGTKEIK 112
DB 81 SGVPRFSGSGGTFTLKISRVEADDDGIYCYMQALQIPLTFGGGTKEIK 112
RESULT 13
Q8TCD0
ID Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 117Z.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
```

```
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW;  FACEDC3A3B03871D CRC64;

Query Match
Best Local Similarity 75.7%; Score 439; DB 2; Length 239;
Matches 83; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
Db 21 DVVMTQSPSLPVTLLGPASISCRSTQSLVSDGNTYLNWFQRPQSPRRLIYKVSNRD 80
QY 61 SGVPRFSGSGSGTDFTLKISRVEADVGIYCMQALQIPLTFGGGTVK 112
Db 81 SGVPRFSGSGSGTDFTLKISRVEADVGIYCMQALQIPLTFGGGTVK 112

RESULT 14
KV2F_MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
TISSUE=Hybridoma;
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst R., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -!- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal A polysaccharide.
DR PIR; A01913; KVM57S.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Complementarity-determining-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match
Best Local Similarity 74.0%; Score 429; DB 1; Length 113;
Matches 84; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
Db 1 DIVMTQSPSLPVTLLGPASISCRSTQSLVSDGNTYLNWFQRPQSPRRLIYKVSNRD 60
QY 61 SGVPRFSGSGSGTDFTLKISRVEADVGIYCMQALQIPLTFGGGTVK 112
Db 61 SGVPRFSGSGSGTDFTLKISRVEADVGIYCMQALQIPLTFGGGTVK 112

Search completed: November 16, 2005, 22:01:55
Job time : 63.7941 secs
```

```
RESULT 15
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Abersold R., Herbst H., Grutter T., Chang J.-Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 2S25.1 specific for the
RT group A-streptococcal polysaccharide."
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -!- FUNCTION: Anti-streptococcal group A carbohydrate antibody.
DR PIR; A01912; KVM517.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Complementarity-determining-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match
Best Local Similarity 73.6%; Score 427; DB 1; Length 113;
Matches 84; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
Db 1 DIVMTQSPSLPVTLLGPASISCRSTQSLVSDGNTYLNWFQRPQSPRRLIYKVSNRD 60
QY 61 SGVPRFSGSGSGTDFTLKISRVEADVGIYCMQALQIPLTFGGGTVK 112
Db 61 SGVPRFSGSGSGTDFTLKISRVEADVGIYCMQALQIPLTFGGGTVK 112

Search completed: November 16, 2005, 22:01:55
Job time : 63.7941 secs
```

www.ck12.org



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 21:41:29 ; Search time 19.0441 Seconds  
(without alignments)  
439.017 Million cell updates/sec

Title: US-10-660-357A-38  
Perfect score: 580  
Sequence: 1 DIVMTQSPSLPVPVGPAS.....CMQALQIPLTGGGKVKVIK 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUTS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	92.4	113	3	US-09-025-769B-15
2	536	92.4	113	4	US-09-490-070A-15
3	536	92.4	113	4	US-09-490-153-15
4	536	92.4	113	4	US-09-490-324-15
5	533	91.9	112	4	US-09-254-180C-9
6	526	90.7	112	1	US-08-331-398A-49
7	526	90.7	112	2	US-08-331-397B-49
8	526	90.7	112	2	US-08-759-804A-49
9	526	90.7	112	3	US-09-227-693-49
10	521	89.8	112	3	US-09-240-274-30
11	519	89.5	113	1	US-08-082-623-4
12	515	88.8	114	3	US-09-025-769B-29
13	515	88.8	114	3	US-09-025-769B-45
14	515	88.8	114	4	US-09-490-070A-29
15	515	88.8	114	4	US-09-490-070A-45
16	515	88.8	114	4	US-09-490-153-29
17	515	88.8	114	4	US-09-490-153-45
18	515	88.8	114	4	US-09-490-324-29
19	515	88.8	114	4	US-09-490-324-45
20	515	88.8	281	3	US-09-025-769B-178
21	515	88.8	281	4	US-09-490-070A-178
22	515	88.8	281	4	US-09-490-153-178
23	515	88.8	281	4	US-09-490-324-178
24	512	88.3	239	4	US-10-000-489-8
25	510	87.9	112	3	US-09-000-088-2
26	509	87.8	108	1	US-08-488-113B-151
27	509	87.8	108	1	US-08-477-484B-151

28	509	87.8	108	1	US-08-107-669D-15	Sequence 15, Appl
29	509	87.8	108	1	US-08-472-788A-15	Sequence 15, Appl
30	509	87.8	108	2	US-08-477-531B-15	Sequence 15, Appl
31	509	87.8	108	2	US-08-646-360-151	Sequence 151, Appl
32	509	87.8	108	2	US-08-082-842A-15	Sequence 15, Appl
33	509	87.8	108	3	US-08-839-765-151	Sequence 151, Appl
34	509	87.8	108	3	US-09-136-389-151	Sequence 151, Appl
35	509	87.8	108	3	US-09-610-838-151	Sequence 151, Appl
36	509	87.8	108	4	US-09-711-485-151	Sequence 151, Appl
37	505	87.1	112	1	US-08-053-171-16	Sequence 16, Appl
38	504	86.9	112	1	US-08-478-039-88	Sequence 88, Appl
39	504	86.9	112	1	US-08-476-349A-88	Sequence 88, Appl
40	499.5	86.1	113	1	US-08-264-093-10	Sequence 10, Appl
41	491	84.7	100	4	US-09-472-087-115	Sequence 115, Appl
42	490	84.5	116	1	US-08-482-882-66	Sequence 66, Appl
43	490	84.5	116	2	US-08-483-389-66	Sequence 66, Appl
44	490	84.5	116	2	US-08-487-113D-66	Sequence 66, Appl
45	490	84.5	116	2	US-08-473-503-66	Sequence 66, Appl

## ALIGNMENTS

RESULT 1  
US-09-025-769B-15  
; Sequence 15, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: linear  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-15

Query Match 92.4%; Score 536; DB 3; Length 113;  
Best Local Similarity 92.0%; Pred. No. 1.7e-46;  
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

[illegible]

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

### RESULT 3

```

US-09-490-153-15
; Sequence 15, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-153-15

```

RESULT 4  
US-03-450-324-15  
; Sequence 15, Application US/09490324  
; Patent No. 6828422  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Iiming  
; Moroney, Simon  
; Plueckthun, Andrea

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-490-324-15  
Query Match 92.4%; Score 536; DB 4; Length 113;  
Best Local Similarity 92.0%; Pred. No. 1.7e-46;  
Matches 103; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 1 DIVMTQSPSLPVPPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
DB 1 DIVMTQSPSLPVPPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
QY 61 SGVPRFSGSGTDTFLKISRVEADDVGYYCMQALQIPLTFGGGKVEIK 112  
DB 61 SGVPRFSGSGTDTFLKISRVEADDVGYYCMQALQIPLTFGGGKVEIK 112

RESULT 5  
US-09-254-180C-9  
Sequence 9, Application US/09254180C  
Patent No. 6777540  
GENERAL INFORMATION:  
APPLICANT: OKUMURA, Ko  
APPLICANT: EDA, Yasuyuki  
APPLICANT: MAEDA, Hiroaki  
APPLICANT: USHIO, Yoshitaka  
APPLICANT: HIGUCHI, Hirofumi  
APPLICANT: NAKATA, Motomi  
TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or  
FILE REFERENCE: 050006-0055  
CURRENT APPLICATION NUMBER: US/09/254,180C  
CURRENT FILING DATE: 1999-04-15  
PRIOR APPLICATION NUMBER: PCT/JP97/02983  
PRIOR FILING DATE: 1997-08-27  
PRIOR APPLICATION NUMBER: 271546/1996  
PRIOR FILING DATE: 1996-09-20  
PRIOR APPLICATION NUMBER: 231472/1996

PRIOR FILING DATE: 1996-09-02  
NUMBER OF SEQ ID NOS: 183  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 9  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-254-180C-9

Query Match 91.9%; Score 533; DB 4; Length 112;  
Best Local Similarity 91.1%; Pred. No. 3.4e-46;  
Matches 102; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
DB 1 DIVMTQSPSLPVPPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
QY 61 SGVPRFSGSGTDTFLKISRVEADDVGYYCMQALQIPLTFGGGKVEIK 112  
DB 61 SGVPRFSGSGTDTFLKISRVEADDVGYYCMQALQIPLTFGGGKVEIK 112

RESULT 6  
US-08-331-398A-49  
Sequence 49, Application US/08331398A  
Patent No. 5608039  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark  
APPLICANT: Fitzgerald, David  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pai, Lee  
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
TITLE OF INVENTION: and Their Uses (as amended)  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,398A  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein

```

; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IGM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-397B-49

Query Match          90.7%; Score 526; DB 1; Length 112;
Best Local Similarity 91.1%; Pred. No. 1.7e-45;
Matches 102; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRDFSGSGGTDTLTKISRVEADVGIIYCMQALQIPLTFGGGKVEIK 112
Db 61 SGVPRDFSGSGGTDTLTKISRVEADVGIIYCMQALQIPLTFGGGKVEIK 112

RESULT 7
US-08-331-397B-49
; Sequence 49, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human Igm antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-397B-49

Query Match          90.7%; Score 526; DB 2; Length 112;
Best Local Similarity 91.1%; Pred. No. 1.7e-45;
Matches 102; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

Best Local Similarity 91.1%; Pred. No. 1.7e-45;
Matches 102; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRDFSGSGGTDTLTKISRVEADVGIIYCMQALQIPLTFGGGKVEIK 112
Db 61 SGVPRDFSGSGGTDTLTKISRVEADVGIIYCMQALQIPLTFGGGKVEIK 112

RESULT 8
US-08-759-804A-49
; Sequence 49, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IGM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-759-804A-49

Query Match          90.7%; Score 526; DB 2; Length 112;
Best Local Similarity 91.1%; Pred. No. 1.7e-45;

```

Matches	102;	Conservative	2;	Mismatches	8;	Indels	0;	Gaps	0;
QY	1	DIVMTQSLPLVP	IGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYIGSNRA	60					
DB	1	DIVMTQSLPLVP	IGPEPASISCRSSQSLHLSNGYNYLDWYLOKPGQSPQLLIYIGSNRA	60					
QY	61	SGVPDRFSGSGGTDFTLKLSRVEADVGIYICMQALQIPLTFGGTKVEIK	112						
DB	61	SGVPDRFSGSGGTDFTLKLSRVEADVGIYICMQGLQTFQTPTGGTKVEIK	112						
RESULT 9									
US-09-227-693-49									
; Sequence 49, Application US/09227693									
; Patent No. 6287562									
; GENERAL INFORMATION:									
; APPLICANT: PASTAN, Ita									
; APPLICANT: BENHAR, Itai									
; APPLICANT: PADLAN, Eduardo A.									
; APPLICANT: JUNG, Sun-Hee									
; APPLICANT: LEE, Byungkook									
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY									
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF									
; NUMBER OF SEQUENCES: 50									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: Townsend and Townsend Khourie and Crew									
; STREET: Steuart Street Tower, One Market Plaza									
; CITY: San Francisco									
; STATE: California									
; COUNTRY: US									
; ZIP: 94105-1493									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: PatentIn Release #1.0, Version #1.25									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/09/227,693									
; FILING DATE:									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: 08/331,396									
; FILING DATE:									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: US 07/767,331									
; FILING DATE: 30-SEP-1991									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: US 0									

```
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-055-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..113
; OTHER INFORMATION: /note= "The peptide sequence of the
; OTHER INFORMATION: V-1 region of SDZ MSL 109"
; US-08-082-623-4

Query Match      89.5%; Score 519; DB 1; Length 113;
Best Local Similarity 89.3%; Pred. No. 8.6e-45;
Matches 100; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLHTNGYNYLDWYVQKPGQSPQLLIYLGASRA 60
QY 61 SGVPRFSGSGGTDFTLKISRVEADDVGYYCQALQIPLTFGGGKVEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADDVGYYCQALQIPLTFGGGKVEIK 112

RESULT 12
US-09-025-769B-29
; Sequence 29, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: US/09/025,769B
; PRIORITY INFORMATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-45

Query Match      88.8%; Score 515; DB 3; Length 114;
Best Local Similarity 89.3%; Pred. No. 2.2e-44;
Matches 100; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-29

Query Match      88.8%; Score 515; DB 3; Length 114;
Best Local Similarity 89.3%; Pred. No. 2.2e-44;
Matches 100; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPPLSLPVIPGEPASISCRSSQSLHTNGYNYLDWYLOKPGQSPQLLIYLGASRA 60
QY 61 SGVPRFSGSGGTDFTLKISRVEADDVGYYCQALQIPLTFGGGKVEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADDVGYYCQALQIPLTFGGGKVEIK 112

RESULT 13
US-09-025-769B-45
; Sequence 45, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: US/09/025,769B
; PRIORITY INFORMATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-45

Query Match      88.8%; Score 515; DB 3; Length 114;
Best Local Similarity 89.3%; Pred. No. 2.2e-44;
Matches 100; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
```

Qy	1	DIWVTSPLPVI	PEPASIS	ICRS	SSOS	LLS	NGNY	LDWY	LQK	QCS	POLL	YIG	SNRA	60
Db	1	DIWVTSPLPVT	PEPASIS	ICRS	SSQS	LLS	NGNY	LDWY	LQK	QCS	POLL	YIG	SNRA	60
Qy	61	SGVDFR	SGSG	STDF	TL	KI	SR	VEAD	DV	GI	YCM	QAL	PI	112
Db	61	SGVDFR	SGSG	STDF	TL	KI	SR	VEAD	DV	GI	YCM	QAL	PI	112

RESULT 14

US-09-490-070A-29  
; Sequence 29, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-490-070A-29

**RESULT 15**

US-09-490-070A-45

```

: Sequence 45, Application US/09490070A
: Patent No. 6696248
: GENERAL INFORMATION:
: APPLICANT: Knappik, Achim
: Pack, Peter
: Ilag, Vic
: Ge, Liming
: Moroney, Simon
: Plueckthun, Andreas
: TITLE OF INVENTION: Protein/(Poly)peptide libraries
: NUMBER OF SEQUENCES: 373
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
: White & McAuliffe
: STREET: 1666 K Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20006
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/490,070A
: FILING DATE: 24-Jan-2000
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: EP 95 11 3021.0
: FILING DATE: 18-AUG-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Colin G. Sandercock, Esq.
: REGISTRATION NUMBER: 31,298
: REFERENCE/DOCKET NUMBER: 37629-0005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 912-2000
: TELEFAX: (202) 912-2020
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 114 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-070A-45

```

Search completed: November 16, 2005, 22:07:22  
Job time : 19.0441 secs

THE END OF THE LINE



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 22:02:09 ; Search time 68.7647 Seconds  
(without alignments)  
681.481 Million cell updates/sec

Title: US-10-660-357A-38  
Perfect score: 580  
Sequence: 1 DIVMTQSPSLPVPFGEPAS.....CMQALQIPLTFGGGKVEIK 112  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues  
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications\_AA.\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	580	100.0	112	14	US-10-330-613-38
2	580	100.0	112	14	Sequence 38, Appl
3	580	100.0	112	16	US-10-330-530-38
4	552	95.2	112	14	US-10-660-357-38
5	552	95.2	112	14	Sequence 38, Appl
6	552	95.2	112	14	US-10-269-805-18
7	548	94.5	262	15	US-10-269-805-26
8	548	94.5	262	15	Sequence 26, Appl
9	547	94.3	112	15	US-10-309-762-33
10	545	94.0	112	14	US-10-309-762-33
11	544	93.8	112	14	US-09-880-748-2081
					Sequence 2081, Ap
					Sequence 32, Appl
					Sequence 2, Appl
					Sequence 44, Appl

12	544	93.8	112	20	US-11-021-715-82	Sequence 82, Appl
13	544	93.8	112	20	US-11-021-715-85	Sequence 85, Appl
14	543	93.6	112	17	US-10-638-265-40	Sequence 40, Appl
15	543	93.6	112	17	US-10-638-265-48	Sequence 48, Appl
16	540	93.1	112	14	US-10-269-805-28	Sequence 28, Appl
17	540	93.1	112	16	US-10-663-244-71	Sequence 71, Appl
18	540	93.1	238	16	US-10-663-244-148	Sequence 148, Appl
19	539.5	93.0	111	14	US-10-041-860-16	Sequence 16, Appl
20	539.5	93.0	111	14	US-10-041-860-220	Sequence 220, Appl
21	539.5	93.0	111	14	US-10-041-860-250	Sequence 254, Appl
22	539.5	93.0	111	14	US-10-041-860-279	Sequence 279, Appl
23	539.5	93.0	111	16	US-10-665-383-12	Sequence 12, Appl
24	539	92.9	112	16	US-10-663-244-59	Sequence 59, Appl
25	539	92.9	112	17	US-10-638-285-60	Sequence 60, Appl
26	539	92.9	238	16	US-10-663-244-144	Sequence 144, Appl
27	538	92.8	112	15	US-10-292-088-103	Sequence 103, Appl
28	538	92.8	112	15	US-10-292-088-111	Sequence 111, Appl
29	538	92.8	112	17	US-10-877-773-30	Sequence 30, Appl
30	538	92.8	112	17	US-10-877-774-30	Sequence 58, Appl
31	538	92.8	112	17	US-10-735-916A-58	Sequence 177, Appl
32	538	92.8	113	15	US-10-308-817-177	Sequence 177, Appl
33	538	92.8	113	15	US-10-453-698-177	Sequence 6, Appl
34	538	92.8	125	14	US-10-010-942B-6	Sequence 6, Appl
35	538	92.8	125	15	US-10-388-389-6	Sequence 6, Appl
36	538	92.8	125	16	US-10-703-713-6	Sequence 6, Appl
37	538	92.8	125	16	US-10-704-070-6	Sequence 6, Appl
38	538	92.8	125	17	US-10-232-030-6	Sequence 6, Appl
39	537	92.6	112	15	US-10-292-088-112	Sequence 112, Appl
40	537	92.6	112	17	US-10-877-773-28	Sequence 28, Appl
41	537	92.6	112	17	US-10-877-773-31	Sequence 31, Appl
42	537	92.6	112	17	US-10-877-773-32	Sequence 32, Appl
43	537	92.6	112	17	US-10-877-773-33	Sequence 33, Appl
44	537	92.6	112	17	US-10-877-774-28	Sequence 28, Appl
45	537	92.6	112	17	US-10-877-774-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1  
US-10-330-613-38  
; Sequence 38, Application US/10330613  
; Publication No. US20030147809A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613-38

Query Match	100.0%;	Score 580;	DB 14;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 7.6e-48;	Mismatches 0;	Indels 0;
Matches 112;	Conservative 0;			Gaps 0;
QY	1	DIVMTQSPSLPVPFGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPOLLILYLSNRA	60	
Db	1	DIVMTQSPSLPVPFGEPASISCRSSQSLQSGNNYLDWYLOKPGQSPOLLILYLSNRA	60	
QY	61	SGVPRFRSGSGGTDTFLKISRVEADVGIIYCMQALQIPLTFGGGKVEIK	112	
Db	61	SGVPRFRSGSGGTDTFLKISRVEADVGIIYCMQALQIPLTFGGGKVEIK	112	
RESULT 2				

```
US-10-330-530-38
; Sequence 38, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-38

Query Match      100.0%; Score 580; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.6e-48;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGTKVEIK 112

RESULT 3
US-10-660-357-38
; Sequence 38, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-38

Query Match      100.0%; Score 580; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.6e-48;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGTKVEIK 112

RESULT 4
US-10-269-805-18
; Sequence 18, Application US/10259805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
```

```
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-18

Query Match      95.2%; Score 552; DB 14; Length 112;
Best Local Similarity 94.6%; Pred. No. 3.7e-45;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGTKVEIK 112

RESULT 5
US-10-269-805-26
; Sequence 26, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-26

Query Match      95.2%; Score 552; DB 14; Length 112;
Best Local Similarity 94.6%; Pred. No. 3.7e-45;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGTKVEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADVGVIYCMQALQIPLTFGGGTKVEIK 112

RESULT 6
US-10-309-762-33
; Sequence 33, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
```

```
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-33

Query Match
Best Local Similarity 95.2%; Score 552; DB 15; Length 112;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
DB 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGNSRA 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112
DB 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112

RESULT 7
US-09-880-748-2081
; Sequence 2081, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2081

Query Match
Best Local Similarity 94.5%; Score 548; DB 15; Length 262;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
DB 150 EIVMTQSPSLPVPVIGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGNSRA 209

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112
DB 210 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 261

RESULT 8
US-10-293-418-2081
; Sequence 2081, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2081

Query Match
Best Local Similarity 94.3%; Score 547; DB 15; Length 112;
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGNSRA 60
DB 1 DIVMTQSPSLPVPVIGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGNSRA 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112
DB 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQIPLTFGGGKVEIK 112
```



; Sequence 40, Application US/10638265  
; Publication No. US20050031614A1  
; GENERAL INFORMATION:  
; APPLICANT: Roskos, Lorin  
; APPLICANT: Foltz, Ian  
; APPLICANT: King, Chadwick  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID  
; FILE REFERENCE: HORMONE (PTH) AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10/638,265  
; CURRENT FILING DATE: 2003-08-08  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homosapien  
US-10-638-265-40

Query Match 93.6%; Score 543; DB 17; Length 112;  
Best Local Similarity 92.9%; Pred. No. 2.7e-44;  
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
DB 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
  
QY 61 SGVPRFSGSGGTDFTLKISRVEADDVGYYCMQALQIPLTFGGGTVKEIK 112  
DB 61 SGVPRFSGSGGTDFTLKISRVEADDVGYYCMQALQIPLTFGGGTVKEIK 112

## RESULT 15

US-10-638-265-48  
; Sequence 48, Application US/10638265  
; Publication No. US20050031614A1  
; GENERAL INFORMATION:  
; APPLICANT: Roskos, Lorin  
; APPLICANT: Foltz, Ian  
; APPLICANT: King, Chadwick  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID  
; FILE REFERENCE: HORMONE (PTH) AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10/638,265  
; CURRENT FILING DATE: 2003-08-08  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homosapien  
US-10-638-265-48

Query Match 93.6%; Score 543; DB 17; Length 112;  
Best Local Similarity 92.9%; Pred. No. 2.7e-44;  
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
DB 1 DIVMTQSPVLPVIGPEPASISCRSSQSLQSGNNYLDWYLOKPGQSPQLLIYLGSNRA 60  
  
QY 61 SGVPRFSGSGGTDFTLKISRVEADDVGYYCMQALQIPLTFGGGTVKEIK 112  
DB 61 SGVPRFSGSGGTDFTLKISRVEADDVGYYCMQALQIPLTFGGGTVKEIK 112

Search completed: November 16, 2005, 23:05:45  
Job time : 68.7647 secs

1. The first group of people who are interested in the results of the study are the researchers themselves. They want to know if the study was successful in achieving its objectives and if the data collected is reliable and valid.